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STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,265  
FILING DATE: 06-Jun-1995

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-08-467-265-17

Query Match  
Best Local Similarity 50.1%; Score 721.5; DB 4: Length 199;  
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISPAWYESTAVI-DOEFKELKLDYRGKYLVEFFYPDLFTVCPEITIAFGRLBE 137  
DB 6 AKIGPAPNFKATVAMPQGFIDISLSEKKGKYYVEFFYPDLFTVCPEITIAFGRLBE 65  
QY 138 FRSINTEVACVDSQFTHLAWINTPROGGIGPRLIPLSDLTHQISKDYGVYEDSGH 197  
DB 66 FKLMCGVIGASVDSHFCHLAWINTPKQGGIGPNNIPILISDPKRTIAQDYGLAADGI 125  
QY 198 TLRLFTIIDDGILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPSSEITI 257  
DB 126 SFRGLFIIDDKGILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPSSEITI 257  
QY 258 PDPAKGLKYEFSK 269  
DB 186 PDVAKSKEYFSK 197

RESULT 9  
Sequence 17, Application US/09407891  
Patent No. 6294164

GENERAL INFORMATION:  
APPLICANT: NI, Jian

APPLICANT: Yu, Guo-liang  
APPLICANT: Gentz, Reiner

APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARBELL, BRNE, BAIN, GILFILLAN, CECCHI,

ADDRESSEE: STUART & OLSTEIN  
STREET: 6 Becker Farm Road  
CITY: Roseland

STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/407,891  
FILING DATE:  
CLASSIFICATION:  
Prior APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,265  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-407-891-17

Query Match  
Best Local Similarity 50.1%; Score 721.5; DB 4: Length 199;  
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISPAWYESTAVI-DOEFKELKLDYRGKYLVEFFYPDLFTVCPEITIAFGRLBE 137  
DB 6 AKIGPAPNFKATVAMPQGFIDISLSEKKGKYYVEFFYPDLFTVCPEITIAFGRLBE 65  
QY 138 FRSINTEVACVDSQFTHLAWINTPROGGIGPRLIPLSDLTHQISKDYGVYEDSGH 197  
DB 66 FKLMCGVIGASVDSHFCHLAWINTPKQGGIGPNNIPILISDPKRTIAQDYGLAADGI 125  
QY 198 TLRLFTIIDDGILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPSSEITI 257  
DB 126 SFRGLFIIDDKGILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPSSEITI 257  
QY 258 PDPAKGLKYEFSK 269  
DB 186 PDVAKSKEYFSK 197

Sequence comparison

RESULT 10  
Sequence 2, Application US/08299162A  
Patent No. 5610286

GENERAL INFORMATION:  
APPLICANT: Shau, Hungyi

APPLICANT: Golub, Sidney H  
TITLE OF INVENTION: Natural Killer Cell Enhancing Factor

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David J. Oldenkamp

STREET: 2029 Century Park East, Suite 3800  
CITY: Los Angeles  
STATE: CA

COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299,162A

FILING DATE: August 31, 1994  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Oldenkamp, David J

REFERENCE/DOCKET NUMBER: 104-280

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TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310-788-5000  
 TELEFAX: 310-277-1297  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-299-162A-2

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 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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 DB 66 FKLNCCVIGASVDSHCHLAWNTPKQGLGPMNIPVSDPKRTIAQDYGVLEKDEGI 125  
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 126 SFKGLFLIDDKGLIRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185  
 QY 258 PDPAGKLTAEFK 269  
 DB 186 PDVPRKTEYFSK 197

RESULT 11  
 US-08-467-265-14  
 Sequence 14, Application US/08467265  
 Patent No. 5985612

GENERAL INFORMATION:  
 APPLICANT: NI, Jian  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,265  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-456  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-467-265-14

Query Match  
 Best Local Similarity 49.5%; Score 713.5; DB 2; Length 199;  
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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 DB 6 AKIHPAPNPKATVMDGQPKDLSIDYRGKYVFFFPIDFTFVCPTEIARGLDEE 65  
 QY 138 FRSLNTEVAVASVDSQFTHLAMINTPRGGLGPIRIRPLSDLTHTQISKDYGVLEDSGH 197  
 DB 66 FKLNCCVIGASVDSHCHLAWNTPKQGLGPMNIPVSDPKRTIAQDYGVLEKDEGI 125  
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 126 SFKGLFLIDDKGLIRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185  
 QY 258 PDPAGKLTAEFK 269  
 DB 186 PDVPRKTEYFSK 197

RESULT 12  
 US-08-467-265-14  
 Sequence 14, Application US/08467265  
 Patent No. 6255079

GENERAL INFORMATION:  
 APPLICANT: NI, Jian  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,265  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-456  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-08-467-265-14

Query Match  
 Best Local Similarity 49.5%; Score 713.5; DB 4; Length 199;  
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:18:18 : Search time 15 seconds

(without alignments)  
531.574 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLLAATTPDHGRHRL.....GSEIIIPDPAKLYFDKLN 271

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BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1441	100.0	271	4	US-08-467-265-2
3	1441	100.0	271	4	US-09-407-891-2
4	740	51.4	198	2	US-08-467-265-15
5	740	51.4	198	4	US-08-467-265-15
6	740	51.4	198	4	US-09-407-891-15
7	721.5	50.1	199	2	US-08-467-265-17
8	721.5	50.1	199	4	US-08-467-265-17
9	721.5	50.1	199	4	US-09-407-891-17
10	713.5	49.5	199	1	US-08-299-162A-2
11	713.5	49.5	199	2	US-08-467-265-14
12	713.5	49.5	199	4	US-08-467-265-14
13	713.5	49.5	199	4	US-09-407-891-14
14	689	47.8	257	2	US-08-467-265-16
15	689	47.8	257	4	US-08-467-265-16
16	689	47.8	257	4	US-09-407-891-16
17	683	47.4	199	1	US-08-602-262-2
18	683	47.4	199	3	US-09-004-716-2
19	619	43.0	178	1	US-08-299-162A-4
20	587	40.7	199	4	US-09-183-861-24
21	587	40.7	199	4	US-09-022-765-24
22	586	40.7	206	4	US-09-183-861-26
23	586	40.7	206	4	US-09-022-765-26
24	462	32.1	202	4	US-09-556-877-92
25	462	32.1	202	4	US-09-620-412C-92
26	457	31.7	195	4	US-09-556-877-65
27	457	31.7	195	4	US-09-620-412C-65

28	457	31.7	196	4	US-09-556-877-294	Sequence 294, App
29	457	31.7	196	4	US-09-620-412C-294	Sequence 294, App
30	386.5	26.8	351	1	US-08-415-751-17	Sequence 17, Appl
31	385.5	26.8	201	1	US-08-415-751-2	Sequence 2, Appl
32	290	20.1	196	4	US-09-134-001C-4601	Sequence 4601, Ap
33	170.5	11.8	235	4	US-08-862-540-2	Sequence 2, Appl
34	170.5	11.8	235	4	US-09-633-043-2	Sequence 2, Appl
35	168	11.7	350	1	US-08-415-751-15	Sequence 15, Appl
36	167.5	11.6	235	4	US-08-862-540-9	Sequence 9, Appl
37	167.5	11.6	235	4	US-09-633-043-9	Sequence 9, Appl
38	137.5	9.5	223	4	US-09-411-578-3	Sequence 3, Appl
39	136.5	9.5	157	4	US-09-134-001C-4714	Sequence 4714, Ap
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41	103.5	7.2	214	4	US-08-959-004-1	Sequence 1, Appl
42	100.5	7.0	144	4	US-08-961-083-44	Sequence 44, Appl
43	96.5	6.7	189	4	US-08-959-004-8	Sequence 8, Appl
44	89.5	6.2	168	4	US-09-134-001C-3764	Sequence 3764, Ap
45	84	5.8	2037	4	US-09-306-998-3	Sequence 3, Appl

## ALIGNMENTS

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RESULT 1
US-08-467-265-2
; Sequence 2, Application US/08467265
; Patent No. 5985612
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESS: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,265
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-265-2

Query Match      100.0%  Score 1441:  DB 2:  Length 271:
Best Local Similarity 100.0%  Pred. No. 2.5e-15;
Matches 271:  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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DB      1 MEALPLLAATTPDHGRHRLLLPLFLPLPGAVGMEETEPRTREECHFYAGGY 60
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DB 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAMINTPRROGGIGPIRIPILSDL 180  
QY 181 THQISKDYGVLIEDSGHILRGILFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
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QY 241 HGEVCPAGKPKGSETIIPDPAGKLYFDKLN 271  
DB 241 HGEVCPAGKPKGSETIIPDPAGKLYFDKLN 271

## RESULT 2

US-08-467-265-2  
Sequence 2, Application US/08467265  
Patent No. 6255079

## GENERAL INFORMATION:

APPLICANT: NI, Jian  
Yu, Guo-Liang  
Gentz, Reiner  
Rosen, Craig A.  
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
STUART & OLSTEIN  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467, 265  
FILING DATE: 06-Jun-1995  
CLASSIFICATION: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 271 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-467-265-2

Query Match 100.0%; Score 1441; DB 4; Length 271;  
Best Local Similarity 100.0%; Pred. No. 2, 5e-157;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEALPPLAATPPDGRHRRLLPLLLFLPAGAVQGMETEBRPTREBCHFYAGGOVY 60  
QY 61 PGEASRVAVADHSHLSKAKISKAPAPWEGTAVIDGFEKELKLTIDYRGKYLVEFFYPIDF 120  
DB 61 PGEASRVAVADHSHLSKAKISKAPAPWEGTAVIDGFEKELKLTIDYRGKYLVEFFYPIDF 120

QY 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAMINTPRROGGIGPIRIPILSDL 180  
DB 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAMINTPRROGGIGPIRIPILSDL 180  
QY 181 THQISKDYGVLIEDSGHILRGILFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
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QY 241 HGEVCPAGKPKGSETIIPDPAGKLYFDKLN 271  
DB 241 HGEVCPAGKPKGSETIIPDPAGKLYFDKLN 271

## RESULT 3

US-09-407-891-2  
Sequence 2, Application US/09407891  
Patent No. 6294164

## GENERAL INFORMATION:

APPLICANT: NI, Jian  
Yu, Guo-Liang  
Gentz, Reiner  
Rosen, Craig A.  
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
STUART & OLSTEIN  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/407, 891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467, 265  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 271 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-407-891-2

Query Match 100.0%; Score 1441; DB 4; Length 271;  
Best Local Similarity 100.0%; Pred. No. 2, 5e-157;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEALPPLAATPPDGRHRRLLPLLLFLPAGAVQGMETEBRPTREBCHFYAGGOVY 60  
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QY 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAMINTPRROGGIGPIRIPILSDL 180



Db 121 TFVCPTEIIAEGDRLEERSINTEVACSVDSQFTHLAWINTPRQGLGPIRLPLSDL 180  
 QY 181 THQISKQYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240  
 Db 181 THQISKQYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSEIIPDPAGKLKYPDKLN 271  
 Db 241 HGEVCPAGMKPGSEIIPDPAGKLKYPDKLN 271

## RESULT 4

US-08-467-265-15  
 : Sequence 15, Application US/08467265  
 : Patent No. 5985612  
 : GENERAL INFORMATION:  
 : APPLICANT: NI, Jian  
 : APPLICANT: Yu, Guo-Liang  
 : APPLICANT: Gentz, Reiner  
 : APPLICANT: Rosen, Craig A.  
 : TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 : NUMBER OF SEQUENCES: 17  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 : ADDRESSEE: STUART & OLSTEIN  
 : STREET: 6 Becker Farm Road  
 : CITY: Roseland  
 : STATE: New Jersey  
 : COUNTRY: USA  
 : ZIP: 07068  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/467,265  
 : FILING DATE: 06-JUN-1995  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Ferraro, Gregory D.  
 : REGISTRATION NUMBER: 36,134  
 : REFERENCE/DOCKET NUMBER: 325800-456  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 201-994-1700  
 : TELEFAX: 201-994-1744  
 : INFORMATION FOR SEQ ID NO: 15:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 198 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-467-265-15

Query Match 51.4%; Score 740; DB 2; Length 198;  
 Best Local Similarly 69.9%; Pred. No. 5.8e-77;

Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKIKPAPYMGCTAVIOSEFEKLTDRGKYLVEFFPLDFTVCPEIIAIFGDRLEEF 138  
 Db 6 ARICKPAPDFRATVVDQAEVKLSDKGKIVVLEFPDFTVCPEIIAIFSRADF 65  
 QY 139 RSINTEVACSVDSQFTHLAWINTPRQGLGPIRLPLSDLTQISKDYGVLEDSGHT 198  
 Db 66 RKLCEVLGVSDSQFNLAWINTPRKRGGLGPIRLPLSDLTQISKDYGVLEDSGHT 125  
 QY 199 LRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMKPGSEIIP 258  
 Db 126 YRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMKPGSEIIP 185  
 QY 259 DPAGKLKYPDKLN 271

Db 186 NVDDSKETFSKHN 198

## RESULT 5

US-08-467-265-15  
 : Sequence 15, Application US/08467265  
 : Patent No. 6255079  
 : GENERAL INFORMATION:  
 : APPLICANT: NI, Jian  
 : APPLICANT: Yu, Guo-Liang  
 : APPLICANT: Gentz, Reiner  
 : APPLICANT: Rosen, Craig A.  
 : TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 : NUMBER OF SEQUENCES: 17  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 : ADDRESSEE: STUART & OLSTEIN  
 : STREET: 6 Becker Farm Road  
 : CITY: Roseland  
 : STATE: New Jersey  
 : COUNTRY: USA  
 : ZIP: 07068  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/467,265  
 : FILING DATE: 06-Jun-1995  
 : CLASSIFICATION: <unknown>  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Ferraro, Gregory D.  
 : REGISTRATION NUMBER: 36,134  
 : REFERENCE/DOCKET NUMBER: 325800-456  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 201-994-1700  
 : TELEFAX: 201-994-1744  
 : INFORMATION FOR SEQ ID NO: 15:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 198 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: <unknown>  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 : US-08-467-265-15

Query Match 51.4%; Score 740; DB 4; Length 198;  
 Best Local Similarly 69.9%; Pred. No. 5.8e-77;

Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKIKPAPYMGCTAVIOSEFEKLTDRGKYLVEFFPLDFTVCPEIIAIFGDRLEEF 138  
 Db 6 ARICKPAPDFRATVVDQAEVKLSDKGKIVVLEFPDFTVCPEIIAIFSRADF 65  
 QY 139 RSINTEVACSVDSQFTHLAWINTPRQGLGPIRLPLSDLTQISKDYGVLEDSGHT 198  
 Db 66 RKLCEVLGVSDSQFNLAWINTPRKRGGLGPIRLPLSDLTQISKDYGVLEDSGHT 125  
 QY 199 LRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMKPGSEIIP 258  
 Db 126 YRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMKPGSEIIP 185  
 QY 259 DPAGKLKYPDKLN 271  
 Db 186 NVDDSKETFSKHN 198

## RESULT 6

US-09-407-891-15  
 : Sequence 15, Application US/09407891



```

1 RESULT 9
2 US-09-407-891-17
3 : Sequence 17, Application US/09407891
4 : Patent No. 6294164
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: NI, Jian
9 :
10 : APPLICANT: YU, Guo-Liang
11 :
12 : APPLICANT: Gentz, Reiner
13 :
14 : APPLICANT: Rosen, Craig A.
15 :
16 : TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
17 :
18 : NUMBER OF SEQUENCES: 17
19 :
20 : CORRESPONDENCE ADDRESS:
21 :
22 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
23 :
24 : ADDRESSEE: STUART & OLSTEIN
25 :
26 : STREET: 6 Becker Farm Road
27 :
28 : CITY: Roseland
29 :
30 : STATE: New Jersey
31 :
32 : COUNTRY: USA
33 :
34 : ZIP: 07068
35 :
36 : COMPUTER READABLE FORM:
37 :
38 : MEDIUM TYPE: Floppy disk
39 :
40 : COMPUTER: IBM PC compatible
41 :
42 : OPERATING SYSTEM: PC-DOS/MS-DOS
43 :

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RESULT 10  
US-08-299-162A-2  
Sequence 2, Application US/08299162A  
Patent No. 5610286  
GENERAL INFORMATION:  
APPLICANT: Shau, Sidney H  
TITLE OF INVENTION: Natural Killer Cell Enhancing Factor  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRES:  
ADDRESSEE: David J. Oldenkamp  
STREET: 2029 Century Park East, Suite 3800  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299,162A  
FILING DATE: August 31, 1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Oldenkamp, David J  
REFERENCE/DOCKET NUMBER: 104-280

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310-788-5000  
 TELEFAX: 310-277-1297  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-299-162A-2

Query Match 49.5%; Score 713.5; DB 1; Length 199;  
 Best Local Similarity 68.8%; Pred. No. 6.5e-74;  
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKIKPAPMEGTAVI-DGEFEKELADYRGKYLVEFFYPDLFTFVCPTEIIAAGRLLEE 137  
 Db 6 AKIGHPAPNFKATVAMPDGOQFKDISLDYRGKYVFFFPDLFTFVCPTEIIASDRAEE 65  
 QY 138 FRSINTEVAVCSVDSQFTHLAWINTPRRQGLGPIRIPLSDLTHQISKDYGVLDESGH 197  
 Db 66 FKKLNCQVIGASVDSHFCHLAWMTPKKQGLGPMNIPLVSDPKRTTAODYGVLADEGI 125  
 QY 198 TLKGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257  
 Db 126 SFRLFIIDDKGILRQITVNDPCCRVSDETLRLVQAFQFTDKHGEVCPAGMKPGSDTIK 185  
 QY 258 PDPAGKLKPYDK 269  
 Db 186 PDVPKTKYFSK 197

RESULT 11  
 US-08-467-265-14

; Sequence 14, Application US/08467265  
 ; Patent No. 5985612

GENERAL INFORMATION:  
 APPLICANT: NI, Jian  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA

ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,265  
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-456  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-467-265-14

Query Match 49.5%; Score 713.5; DB 2; Length 199;  
 Best Local Similarity 68.8%; Pred. No. 6.5e-74;  
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKIKPAPMEGTAVI-DGEFEKELADYRGKYLVEFFYPDLFTFVCPTEIIAAGRLLEE 137  
 Db 6 AKIGHPAPNFKATVAMPDGOQFKDISLDYRGKYVFFFPDLFTFVCPTEIIASDRAEE 65  
 QY 138 FRSINTEVAVCSVDSQFTHLAWINTPRRQGLGPIRIPLSDLTHQISKDYGVLDESGH 197  
 Db 66 FKKLNCQVIGASVDSHFCHLAWMTPKKQGLGPMNIPLVSDPKRTTAODYGVLADEGI 125  
 QY 198 TLKGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257  
 Db 126 SFRLFIIDDKGILRQITVNDPCCRVSDETLRLVQAFQFTDKHGEVCPAGMKPGSDTIK 185  
 QY 258 PDPAGKLKPYDK 269  
 Db 186 PDVPKTKYFSK 197

RESULT 12  
 US-08-467-265-14

; Sequence 14, Application US/08467265  
 ; Patent No. 6255079

GENERAL INFORMATION:  
 APPLICANT: NI, Jian  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Gentz, Reiner  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA

ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,265  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-456  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-08-467-265-14

Query Match 49.5%; Score 713.5; DB 4; Length 199;  
 Best Local Similarity 68.8%; Pred. No. 6.5e-74;  
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;



Db 246 TASKKEYEKVH 256

RESULT 15

US-08-467-265-16

Sequence 16, Application US/08467265

Patent No. 6255079

GENERAL INFORMATION:

APPLICANT: NI, Jian

Yu, Guo-Liang

Gentz, Reiner

Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 17

ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265

FILING DATE: 06-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-08-467-265-16

Query Match 47.88; Score 689; DB 4; Length 257;

Best Local Similarity 64.48; Pred. No. 6.3e-71;

Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAPYMEGTAVIDGCEKELKLTIDYGRKYLFFEFYPLDFTFVCPTETIARGLRLEPRS 140  
Db 66 VTQHAPYFKGTAAVNVNGEFKELSLDDEKGYIVLEFFYPLDFTFVCPTETIARGLRLEPRS 125  
QY 141 INTEVAVACSVDSOFTHLAMINTPRRGGLGPIRIPLSLTHQISKDYGVYLEDGHTLR 200  
Db 126 VNCEVVAVSVDHSRSHLAWITPRKNGLGHMNTLLSDITKQISRDYGVYLEDGHTLR 185  
QY 201 GLFTIIDKGLRQTLNDLPGRSVDETLLRKYAFQYTDKHGEVCPAGWKPGSETITPDP 260  
Db 186 GLFTIIDNGVYKHLSDVNDLPGRSVETLRLVKAFOFVETHGEVCPANWTPESTIKRSP 245  
QY 261 AGKLKYPDKLN 271  
Db 246 TASKKEYEKVH 256

Search completed: January 17, 2003, 19:19:59  
Job time: 17 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:18:27 : Search time 13 Seconds  
(without alignments)  
414.391 Million cell updates/sec

Title: US-09-911-346-2  
Perfect score: 1441  
Sequence: 1 MEALPLLAATPDPHGRHRL.....GSETIIPDACKLKYFDKLN 271

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database: Published.Applications\_AA:\*

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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	271	10 US-09-911-346-2	Sequence 2, Appl
2	750.5	52.1	233	10 US-09-925-301-973	Sequence 973, Appl
3	740	51.4	198	10 US-09-911-346-15	Sequence 15, Appl
4	721.5	50.1	199	10 US-09-911-346-17	Sequence 17, Appl
5	713.5	49.5	199	10 US-09-911-346-14	Sequence 14, Appl
6	703	48.8	224	10 US-09-925-300-1537	Sequence 1537, Ap
7	689	47.8	257	10 US-09-911-346-16	Sequence 16, Appl
8	598	41.5	926	9 US-09-991-496-128	Sequence 128, Appl
9	598	41.5	925	9 US-09-991-496-127	Sequence 127, Appl
10	598	41.5	982	9 US-09-991-496-95	Sequence 95, Appl
11	598	41.5	982	10 US-09-874-923-95	Sequence 95, Appl
12	598	41.5	1427	9 US-09-991-496-97	Sequence 97, Appl
13	598	41.5	1427	10 US-09-874-923-97	Sequence 97, Appl
14	598	41.5	1641	9 US-09-991-496-96	Sequence 96, Appl
15	598	41.5	1641	10 US-09-874-923-96	Sequence 96, Appl
16	591	41.0	446	9 US-10-025-380-1121	Sequence 1121, Ap
17	591	41.0	446	10 US-09-922-217-1121	Sequence 1121, Ap
18	591	41.0	1464	9 US-10-012-896-1008	Sequence 1008, Ap
19	587	40.7	199	9 US-09-991-496-24	Sequence 24, Appl

20	587	40.7	199	10 US-09-874-923-24	Sequence 24, Appl
21	586	40.7	206	9 US-09-991-496-26	Sequence 26, Appl
22	586	40.7	206	10 US-09-874-923-26	Sequence 26, Appl
23	478	33.2	114	10 US-09-819-505-7	Sequence 7, Appl
24	474	32.9	114	10 US-09-819-505-8	Sequence 8, Appl
25	462	32.1	202	10 US-09-841-133-92	Sequence 92, Appl
26	457	31.7	195	10 US-09-841-133-65	Sequence 65, Appl
27	457	31.7	196	10 US-09-841-133-294	Sequence 294, Appl
28	455	31.6	195	12 US-10-007-693-101	Sequence 101, Appl
29	444	30.8	116	12 US-10-007-693-76	Sequence 76, Appl
30	425	29.5	114	10 US-09-819-505-6	Sequence 6, Appl
31	403	28.0	198	10 US-09-815-242-11459	Sequence 11459, A
32	358	24.8	187	10 US-09-815-242-10591	Sequence 10591, A
33	333	23.1	187	10 US-09-815-242-10081	Sequence 10081, A
34	328	22.8	187	10 US-09-815-242-13714	Sequence 13714, A
35	326	22.6	187	10 US-09-815-242-11776	Sequence 11776, A
36	323.5	22.4	126	10 US-09-925-300-1753	Sequence 1753, Ap
37	314	21.8	126	10 US-09-925-300-1445	Sequence 1445, Ap
38	279	19.4	189	10 US-09-815-242-5318	Sequence 5318, Ap
39	279	19.4	189	10 US-09-815-242-13409	Sequence 13409, A
40	279	19.4	189	10 US-09-815-242-12752	Sequence 12752, A
41	279	19.4	189	10 US-09-815-242-13142	Sequence 13142, A
42	201	13.9	50	10 US-09-864-761-41230	Sequence 41230, A
43	179.5	12.5	224	10 US-09-728-914-37	Sequence 37, Appl
44	172	11.9	224	10 US-09-819-505-4	Sequence 4, Appl
45	171.5	11.9	224	9 US-09-981-553-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-911-346-2  
; Sequence 2, Application US/09911346  
; Patent No. US20020106323A1  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
Yu, Guo-Liang  
Gentz, Reiner  
Rosen, Craig A.  
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CABELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
STUART & OLSTEIN  
STREET: 6 Becker Farm Road  
City: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/911,346  
FILING DATE: 24-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,265  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferrara, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 271 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-09-911-346-2

Query Match 100.0%; Score 1441; DB 10; Length 271;  
Best Local Similarity 100.0%; Pred. No. 5,7e-139;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATPDHGRHRLRLPLLEFLPAGAVQNETERPTRECHFYAGGQVY 60  
DB 1 MEALPLAATPDHGRHRLRLPLLEFLPAGAVQNETERPTRECHFYAGGQVY 60  
QY 61 PGASRSVADHSLHLSKAKISKPAPYWEQVAVDGEKELTDYRKYLVFFFPYLD 120  
DB 61 PGASRSVADHSLHLSKAKISKPAPYWEQVAVDGEKELTDYRKYLVFFFPYLD 120  
QY 121 TVCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDL 180  
DB 121 TVCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDL 180  
QY 181 THQISKYGYVLEDSGHTLRLGFLITLNDLPVGRSVDETLRLVQAFQYTDK 240  
DB 181 THQISKYGYVLEDSGHTLRLGFLITLNDLPVGRSVDETLRLVQAFQYTDK 240  
QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271  
DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

## RESULT 2

US-09-925-301-973  
Sequence 973, Application US/09925301  
Patent No. US20020052308A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 973  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (3)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-301-973

Query Match 52.1%; Score 750.5; DB 10; Length 233;  
Best Local Similarity 67.1%; Pred. No. 7,9e-69;  
Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY 64 ASRVAVADHSLHLSKAKISKPAPYWEQVAVDGEKELTDYRKYLVFFFPYLD 122  
DB 25 ATCVGADADKSSGNKIKHPAPNFKATVMPDQKDISLSYKGYVFFFPYLD 84  
QY 123 VCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDL 182  
DB 85 VCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDL 182  
QY 183 THQISKYGYVLEDSGHTLRLGFLITLNDLPVGRSVDETLRLVQAFQYTDK 242  
DB 145 THQISKYGYVLEDSGHTLRLGFLITLNDLPVGRSVDETLRLVQAFQYTDK 242  
QY 243 HGEVCPAGMKPGSETIIPDPAGKLYFDK 269

DB 205 EVCPAGMKPGSDTIKPDVOKSEYFSK 231

## RESULT 3

US-09-911-346-15  
Sequence 15, Application US/09911346  
Patent No. US20020106323A1  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
Yu, Guo-Liang  
Genetz, Reiner  
Rosen, Craig A.  
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
STUART & OLSTEIN  
STREET: 6 Becker Farm Road  
STATE: New Jersey  
CITY: Roseland  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/911,346  
FILING DATE: 24-Jul-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,265  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-456  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-911-346-15

Query Match 51.4%; Score 740; DB 10; Length 198;  
Best Local Similarity 69.9%; Pred. No. 7,3e-68;  
Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKISKPAPYWEQVAVDGEKELTDYRKYLVFFFPYLDFTVCPTEIIAFGRLEEF 138  
DB 6 ARIGKPAPEFKATVAVDGAFFKELSDYKGYVFFFPYLDFTVCPTEIIAFGRLEEF 65  
QY 139 RSTINTEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDLTHQISKYGYVLEDSGHT 198  
DB 66 RKGCEVAVCSVDQFTHLAMINTPRROGLGPIRLPLSDLTHQISKYGYVLEDSGHT 125  
QY 199 LAGLFIIDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 258  
DB 126 YRGLFIIDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 185  
QY 259 DPAGKLYFDKLN 271  
DB 186 NVDDSKSEYFSKH 198



```

RESULT 4
US-09-911-346-17
; Sequence 17, Application US/09911346
; Patent No. US20020106323A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Yu, Guo-liang
; Gentz, Reiner
; Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,346
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-911-346-17

Query Match          50.1%; Score 721.5; DB 10; Length 199;
Best Local Similarity 68.8%; Pred. No. 5,6e-66;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISKAPWYEGTAVI-DGEFKELKLTDRGKYLVEFFYPLDFTFVCPTEIIAFGRLEE 137
   ||| ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
Db 6 AKIGYAPNPKATVAMPDGGFKDISLSEYKGVVEFFYPLDFTFVCPTEIIAFSDRAE 65

QY 138 FRSINTEVAVCSVDQFTHLAWINTPRGGLPIRIPILSDLTHTQISKDYGYLSDSGH 197
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 66 FKKLNCQVIGASVDSHCHLAWINTPRKOGGLPMNIPILSDPKRTIAQDYGLKADDEGI 125

QY 198 TLRGLEFIIDDKGILRQITLNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
   : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 126 SFGGLFTIIDDKGILRQITLNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185

QY 258 PDPAGKRLKYFDK 269
   || : || :
Db 186 PDVAKSKKEYFSK 197

RESULT 5
US-09-911-346-14
; Sequence 14, Application US/09911346
; Patent No. US20020106323A1

```

```

; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Yu, Guo-liang
; Gentz, Reiner
; Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,346
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-911-346-14

Query Match          49.5%; Score 713.5; DB 10; Length 199;
Best Local Similarity 68.8%; Pred. No. 3.7e-65;
Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISKAPWYEGTAVI-DGEFKELKLTDRGKYLVEFFYPLDFTFVCPTEIIAFGRLEE 137
   ||| ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
Db 6 AKIGYAPNPKATVAMPDGGFKDISLSDYKGVVEFFYPLDFTFVCPTEIIAFSDRAE 65

QY 138 FRSINTEVAVCSVDQFTHLAWINTPRGGLPIRIPILSDLTHTQISKDYGYLSDSGH 197
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 66 FKKLNCQVIGASVDSHCHLAWINTPRKOGGLPMNIPILSDPKRTIAQDYGLKADDEGI 125

QY 198 TLRGLEFIIDDKGILRQITLNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
   : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 126 SFGGLFTIIDDKGILRQITLNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185

QY 258 PDPAGKRLKYFDK 269
   || : || :
Db 186 PDVAKSKKEYFSK 197

RESULT 6
US-09-925-300-1537
; Sequence 1537, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; Applicant: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

```





Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGTGLTMAIPMLADTKTARSYGV 125  
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250  
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVEEVLRLLEAFQVEKHGEVCPANMK 185  
 QY 251 PGSETIIPDPAGKLK-YFDK 269  
 Db 186 KGAPTMKPEPNASVEGYFSK 205

## RESULT 12

US-09-991-496-97  
 ; Sequence 97, Application US/09991496  
 ; Patent No. US20020169285A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Campos-Neto, Antonio  
 ; APPLICANT: Webb, John R.  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Bhatia, Ajay  
 ; APPLICANT: Coler, Rhea  
 ; APPLICANT: Probst, Peter  
 ; APPLICANT: Brannon, Mark  
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE  
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS  
 ; CURRENT APPLICATION NUMBER: US/09/991,496  
 ; CURRENT FILING DATE: 2001-11-20  
 ; NUMBER OF SEQ ID NOS: 137  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 97  
 ; LENGTH: 1427  
 ; TYPE: PRF  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple  
 ; OTHER INFORMATION: Leishmania antigens  
 ; US-09-991-496-97

Query Match 41.5%; Score 598; DB 9; Length 1427;  
 Best Local Similarity 54.0%; Pred. No. 3,1e-52;  
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLSKAKISKRPAYWEGTAVI-DGEFEKELTDYRGKYLVEFFYPDLDTFVCPTETIA 130  
 Db 6 HMSCGNKAKINSPAPSEFEVALMPNGSFKKISLSYKGMVVLFFPYLDFTFVCPTETIA 65  
 QY 131 FGDRLEEFSSINTEVAVCSVDSQFTHLAINTPRROGGGLGPIRIPILSLDTHQISKDYGV 190  
 Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGTGLTMAIPMLADTKTARSYGV 125  
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250  
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVEEVLRLLEAFQVEKHGEVCPANMK 185  
 QY 251 PGSETIIPDPAGKLK-YFDK 269  
 Db 186 KGAPTMKPEPNASVEGYFSK 205

## RESULT 13

US-09-874-923-97  
 ; Sequence 97, Application US/09874923  
 ; Patent No. US20020081320A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Campos-Neto, Antonio  
 ; APPLICANT: Webb, John R.  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Bhatia, Ajay

; APPLICANT: Coler, Rhea  
 ; APPLICANT: Probst, Peter  
 ; APPLICANT: Brannon, Mark  
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE  
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS  
 ; CURRENT APPLICATION NUMBER: US/09/874,923  
 ; CURRENT FILING DATE: 2001-06-04  
 ; NUMBER OF SEQ ID NOS: 122  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 97  
 ; LENGTH: 1427  
 ; TYPE: PRF  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple  
 ; OTHER INFORMATION: Leishmania antigens  
 ; US-09-874-923-97

Query Match 41.5%; Score 598; DB 10; Length 1427;  
 Best Local Similarity 54.0%; Pred. No. 3,1e-52;  
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLSKAKISKRPAYWEGTAVI-DGEFEKELTDYRGKYLVEFFYPDLDTFVCPTETIA 130  
 Db 6 HMSCGNKAKINSPAPSEFEVALMPNGSFKKISLSYKGMVVLFFPYLDFTFVCPTETIA 65  
 QY 131 FGDRLEEFSSINTEVAVCSVDSQFTHLAINTPRROGGGLGPIRIPILSLDTHQISKDYGV 190  
 Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGTGLTMAIPMLADTKTARSYGV 125  
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250  
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVEEVLRLLEAFQVEKHGEVCPANMK 185  
 QY 251 PGSETIIPDPAGKLK-YFDK 269  
 Db 186 KGAPTMKPEPNASVEGYFSK 205

## RESULT 14

US-09-991-496-96  
 ; Sequence 96, Application US/09991496  
 ; Patent No. US20020169285A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Campos-Neto, Antonio  
 ; APPLICANT: Webb, John R.  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Bhatia, Ajay  
 ; APPLICANT: Coler, Rhea  
 ; APPLICANT: Probst, Peter  
 ; APPLICANT: Brannon, Mark  
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE  
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS  
 ; CURRENT APPLICATION NUMBER: US/09/991,496  
 ; CURRENT FILING DATE: 2001-11-20  
 ; NUMBER OF SEQ ID NOS: 137  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 96  
 ; LENGTH: 1641  
 ; TYPE: PRF  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple  
 ; OTHER INFORMATION: Leishmania antigens  
 ; US-09-991-496-96

Query Match 41.5%; Score 598; DB 9; Length 1641;  
 Best Local Similarity 54.0%; Pred. No. 3,8e-52;  
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

[illegible]

## RESULT 15

```

: US-09-874 -923 -96
: Sequence 96, Application US/09874923
: Patent No. US20020081320A1
: GENERAL INFORMATION:
: APPLICANT: Reed, Steven G.
: APPLICANT: Campos-Neto, Antonio
: APPLICANT: Webb, John R.
: APPLICANT: Dillon, David C.
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Bhatia, Ajay
: APPLICANT: Cole, Rhea
: APPLICANT: Probst, Peter
: APPLICANT: Brannon, Mark
: TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
: FILE REFERENCE: 210121.42008
: CURRENT APPLICATION NUMBER: US/09/874,923
: CURRENT FILING DATE: 2001-06-04
: NUMBER OF SEQ ID NOS: 122
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 96
: LENGTH: 1641
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
: OTHER INFORMATION: Leishmania antigens
: US-09-874 -923 -96

```

Query Match	41.5%	Score 598	DB 10	Length 1641
Best Local Similarity	54.0%	Pred. No. 3.8e-52		
Matches 108	Conservative 39	Mismatches 51	Indels 2	Gaps 2

[illegible]

Search completed: January 17, 2003, 19:20:23  
Job time : 18 secs

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GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: January 17, 2003, 19:17:48 : Search time 19 Seconds

(without alignments)  
1371.180 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441  
Sequence: 1 MEALPLLAATTPDHGRHRL.....GSEFTIPDPAGKLYPDKLN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR-73:\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	2	G01790
2	744	51.6	198	2	A57716
3	740	51.4	198	2	I68897
4	735.5	51.0	199	2	A46711
5	731.5	50.8	200	2	I51016
6	730.5	50.7	199	2	I52425
7	721.5	50.1	199	2	A48513
8	701	48.6	576	2	T16005
9	689	47.8	257	2	JQ0064
10	680	47.2	195	2	JC2258
11	639.5	44.4	226	2	S43598
12	634	44.0	192	2	T41413
13	588.5	40.8	203	2	A12385
14	588.5	40.8	210	2	T06318
15	584	40.5	265	2	A47362
16	582.5	39.6	200	2	S76284
17	570.5	39.6	200	2	S76284
18	568.5	39.5	242	2	S49173
19	567	39.3	196	2	S69732
20	548	38.0	199	2	S73193
21	479.5	33.3	233	2	S67947
22	477	33.1	200	2	S29119
23	474.5	32.9	199	2	F83540
24	474.5	32.9	273	2	A43862
25	474.5	32.9	202	2	C97756
26	467	32.4	200	2	G83204
27	461	31.6	195	2	G71492
28	455	31.6	200	2	AB0552
29	451.5	31.3	200	2	AB0552

30	444	30.8	196	2	H85587	thio-specific anti
31	444	30.8	196	2	E72036	thio-specific anti
32	441.5	30.6	180	2	B69867	2-cys peroxidase
33	440.5	30.6	200	2	AB0388	probable alkyl hyd
34	434.5	30.2	183	2	A83983	2-cys peroxidase
35	434.5	30.2	207	2	E82287	antioxidant, Ahpc/
36	432.5	30.0	198	2	B81453	alkyl hydroperoxid
37	406.5	28.2	181	2	AD1275	2-cys peroxidase
38	406.5	28.2	181	2	AD1638	2-cys peroxidase
39	404	28.0	198	2	H71601	probable peroxidase
40	403	28.0	198	2	C64715	alkyl hydroperoxid
41	398.5	27.7	197	2	C84951	alkyl hydroperoxid
42	394.5	27.4	204	2	S78299	hypothetical prote
43	346.5	24.0	206	2	G82668	subunit C of alkyl
44	342	23.7	188	2	D71314	probable alkyl hyd
45	341	23.7	222	2	E70374	alkyl hydroperoxid

## ALIGNMENTS

```
RESULT 1
G01790
probable thiol-specific reductase (EC 1.-.-.-) AOE37-2 - human
N:Alternate names: antioxidant enzyme AOE37-2
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence-revision 06-Jun-1997 #text-change 11-Jun-1999
C:Accession: G01790
R:jin, D.
submitted to the EMBL Data Library, April 1995
A:Reference number: G08418
A:Accession: G01790
A>Status: translated from GB/EMBL/DDB3
A:Molecule type: mRNA
A:Residues: 1-271 <JIN>
A:Cross-references: EMBL:U25182; NID:9799380; PIDN:AB95175.1; PID:9799381
C:Superfamily: alkyl hydroperoxidase reductase c22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase
F:88-229/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match      100.0%; Score 1441; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 1e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEALPLLAATTPDHGRHRLLLPLLPAGAVOGMETEERTRTEECHEFTAGGCVY 60
Db 1 MEALPLLAATTPDHGRHRLLLPLLPAGAVOGMETEERTRTEECHEFTAGGCVY 60
OY 61 PGEASRVSVADSHLSLSKAKISKAPYWEGRFAVDGEFEKELTDYNGKYLVEFFYPLDF 120
Db 61 PGEASRVSVADSHLSLSKAKISKAPYWEGRFAVDGEFEKELTDYNGKYLVEFFYPLDF 120
OY 121 TFVCPTEIIAAGDRLEEFERSINTEVAVCSVDQFTHLAMINTPRROGGLRIRIPLSLD 180
Db 121 TFVCPTEIIAAGDRLEEFERSINTEVAVCSVDQFTHLAMINTPRROGGLRIRIPLSLD 180
OY 181 THQISKDYGVLVEDSGHRLKGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
Db 181 THQISKDYGVLVEDSGHRLKGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
OY 241 HGEVCPAGMKRGSEFTIIPDPAGKLYPDKLN 271
Db 241 HGEVCPAGMKRGSEFTIIPDPAGKLYPDKLN 271

RESULT 2
A57716
thiol-specific antioxidant - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Feb-1996 #sequence-revision 23-Feb-1996 #text-change 11-Jun-1999
C:Accession: A57716
R:Chae, H.-J.; Robison, K.; Poole, L.B.; Church, G.; Storz, G.; Rhee, S.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 7017-7021, 1994
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C:Accession: I51016  
 R:Tabata, T.; Kamio, K.; Tajima, T.; Kaneda, T.; Suzuki, A.  
 Roux's Arch. Dev. Biol. 204, 400-405, 1995  
 A:Title: Bag gene-like protein (Abp-25) of Cynops embryo: regional distribution and gene  
 A:Reference number: I51016  
 A:Accession: I51016  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-200 <TAB>  
 A:Cross-references: GB:D37808; NID:g520852; PIDN:BA07054.1; PID:g520853  
 C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot  
 F:15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 50.8%; Score 731.5; DB 2; Length 200;  
 Best Local Similarity 71.5%; Pred. No. 1.1e-59;  
 Matches 138; Conservative 22; Mismatches 32; Indels 1; Gaps 1;

Qy 78 KAKISRPAYWEGTAVI-DGEFEKELKLDYRGKYLVEFFYPPLDFTVCPTETIAFGDRLE 136  
 Db 5 KAOIGKPAPEFOAKVMGEGEKDKIKLADYRGKYVFFFPPLDFTVCPTETIAFSDBAE 64  
 Qy 137 EFRSINTVACSVDSOTHLAMINTPRQGGIGPIRILPLSLDTHQISKDYGVLEDSG 196  
 Db 65 EFRKINCELIAASVDSHCHLAWMTSRKEGSGMKIPLVADTKRTISODYGVLEDEG 124  
 Qy 197 HTLNGLIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDKHEVCAPGMRKPSERT 256  
 Db 125 ISFRGLFIIDDKGILROITINDLPVGRSVDETLRLVOAFQHTDKGECVCPAGMKPSDTI 184  
 Qy 257 ITPDPAGKLYFDK 269  
 Db 185 KPDISKSEYFSK 197

RESULT 6  
 152425  
 probable thioredoxin peroxidase (EC 1.11.1.-) HBP23 - rat  
 N:Alternate names: heme-binding 23k protein (HBP23); proliferation associated protein P  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 02-Jun-2000  
 C:Accession: I52425  
 R:Iwahara, S.  
 Biochemistry 34, 13398-13406, 1995  
 A:Title: Purification, characterization, and cloning of a heme-binding protein (23 kDa)  
 A:Reference number: I52425; MUID:96027454; PMID:7577926  
 A:Accession: I52425  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-199 <IWA>  
 A:Cross-references: GB:D30035; NID:g1060976; PIDN:BA06275.1; PID:g1060977  
 C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot  
 C:Keywords: heme; oxidoreductase  
 F:15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 50.7%; Score 730.5; DB 2; Length 199;  
 Best Local Similarity 70.3%; Pred. No. 1.4e-59;  
 Matches 135; Conservative 24; Mismatches 32; Indels 1; Gaps 1;

Qy 79 AKISRPAYWEGTAVI-DGEFEKELKLDYRGKYLVEFFYPPLDFTVCPTETIAFGDRLE 137  
 Db 6 AKIGHAPSPFKATAVMPDGOFKDISLSEYKGYVFFFPPLDFTVCPTETIAFSDBAE 65  
 Qy 138 FRSINTEVACSVDSOFTHLAMINTPRQGGIGPIRILPLSLDTHQISKDYGVLEDSG 197  
 Db 66 FKLKLCQYIGASVDSHFCHLAWINTPKQGGIGPMNIPILVSPKRTIADYGVLEDSG 125  
 Qy 198 TLKGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDKHEVCAPGMRKPSERT 257  
 Db 126 SFRGLFIIDDKGILROITINDLPVGRSVDETLRLVOAFQFTKHGEVCPAGMKPSDTIK 185  
 Qy 258 PDPAGKLYFDK 269  
 Db 186 PDVNSKSEYFSK 197

RESULT 7  
 A48513  
 macrophage 23k stress-induced protein - mouse

N:Alternate names: MSP23; osteoblast specific factor 3  
 C:Species: Mus musculus (house mouse)  
 C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Jun-2000  
 A:Accession: A48513; J02259  
 R:Itshii, T.; Yamada, M.; Sato, H.; Matsue, M.; Taketani, S.; Nakayama, K.; Sugita, Y.  
 J. Biol. Chem. 268, 18633-18636, 1993  
 A:Title: Cloning and characterization of a 23-kDa stress-induced mouse peritoneal mac  
 A:Reference number: A48513; MUID:93366771; PMID:8360158  
 A:Accession: A48513  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-199 <ISH>

A:Cross-references: GB:D16142; NID:g286102; PIDN:BA03713.1; PID:g303690  
 A:Experimental source: peritoneal macrophages  
 A>Note: authors translated the codon TGG for residue 177 as Thr, and CAG for residue  
 R:Kawai, S.; Takeshita, S.; Okazaki, M.; Kikuno, K.; Kudo, A.; Amann, E.  
 J. Biochem. 115, 641-643, 1994

A:Note: authors suggest a role in an oxidoreductase reaction system in mammalian cell  
 A:Title: Cloning and characterization of OSF-3, a new member of the MERS family, expr  
 A:Reference number: J02259; MUID:94375405; PMID:8089076  
 A:Accession: J02259  
 A:Molecule type: mRNA  
 A:Residues: 1-199 <KAW>

A:Cross-references: DBJ:D21252; NID:g666969; PIDN:BA04796.1; PID:g666970  
 A:Experimental source: osteoblastic cell line MC3T3-E1  
 A>Note: authors suggest, on the basis of homology to MERS family, that this protein p  
 C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p  
 C:Keywords: glycoprotein  
 F:15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>  
 F:189/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 50.1%; Score 721.5; DB 2; Length 199;  
 Best Local Similarity 68.8%; Pred. No. 9.2e-59;  
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

Qy 79 AKISRPAYWEGTAVI-DGEFEKELKLDYRGKYLVEFFYPPLDFTVCPTETIAFGDRLE 137  
 Db 6 AKIGHAPSPFKATAVMPDGOFKDISLSEYKGYVFFFPPLDFTVCPTETIAFSDBAE 65  
 Qy 138 FRSINTEVACSVDSOFTHLAMINTPRQGGIGPIRILPLSLDTHQISKDYGVLEDSG 197  
 Db 66 FKLKLCQYIGASVDSHFCHLAWINTPKQGGIGPMNIPILVSPKRTIADYGVLEDSG 125  
 Qy 198 TLKGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDKHEVCAPGMRKPSERT 257  
 Db 126 SFRGLFIIDDKGILROITINDLPVGRSVDETLRLVOAFQFTKHGEVCPAGMKPSDTIK 185  
 Qy 258 PDPAGKLYFDK 269  
 Db 186 PDVNSKSEYFSK 197

RESULT 8  
 T16005  
 hypothetical protein F09E5.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 A:Accession: T16005  
 R:Chissole, S.  
 submitted to the EMBL Data Library, September 1995  
 A:Description: The sequence of C. elegans cosmid F09E5.  
 A:Reference number: Z18444  
 A:Accession: T16005  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-576 <CHI>  
 A:Cross-references: EMBL:U37429; NID:g1019949; PID:AA079342.1; CESP:F0  
 A:Experimental source: Strain Bristol N2



[illegible]



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:15:03 ; Search time 39 Seconds  
(without alignments)  
925.921 Million cell updates/sec

Title: US-09-911-346-2  
Perfect score: 1441  
Sequence: 1 MEALPLAATPDHGHNRRL.....GSETIIPDAGKLYPDKIN 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470.

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq.-101002:\*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	271	18 AAW12692	Natural killer cell
2	1441	100.0	271	21 AAY43399	Human natural kill
3	1441	100.0	271	22 AAM50249	Human natural kill
4	1441	100.0	271	22 AAB82478	Natural killer cell
5	1441	100.0	271	22 AAB68038	Amino acid sequenc
6	854.5	59.3	242	22 ABB57947	Drosophila melanog
7	750.5	52.1	233	21 AAB43528	Human cancer assoc
8	750.5	52.1	233	23 ABB41353	Human ovarian anti
9	746	51.8	198	22 AAB68036	Amino acid sequenc
10	721	50.0	198	22 AAB68040	Amino acid sequenc

11	719	49.9	198	21 AAU78580	Mouse peroxiredoxi
12	715	49.6	194	22 ABB58322	Drosophila melanog
13	715	49.6	194	22 ABB58323	Drosophila melanog
14	713.5	49.5	199	18 AAM09793	Natural killer cell
15	703	48.8	224	21 AAB56959	Human prostate can
16	703	48.8	256	22 AAB68037	Amino acid sequenc
17	691	48.0	219	22 ABB26215	Novel human diagno
18	682	47.3	199	18 AAM73715	Drosophila melanog
19	650	45.1	220	22 ABB61843	Natural killer cell
20	637.5	44.2	181	14 AAB39938	NKEF sequence dedu
21	619	43.0	178	18 AAM09794	Natural killer cel
22	598	41.5	982	23 AAU71855	Leishmania antigen
23	598	41.5	1427	23 AAU71857	Leishmania MAP5A-
24	598	41.5	1641	23 AAU71856	Leishmania antigen
25	587	40.7	199	19 AAM70221	Leishmania antigen
26	587	40.7	199	23 ABB60873	Leishmania antigen
27	587	40.7	199	23 AAU71817	Leishmania antigen
28	586	40.7	206	19 AAM70222	Leishmania antigen
29	586	40.7	206	23 ABB60874	Leishmania antigen
30	586	40.7	206	23 AAU71818	Leishmania antigen
31	580	40.2	196	22 ABB62769	Drosophila melanog
32	571	39.6	271	21 AAG23833	Arabidopsis thalia
33	571	39.6	271	21 AAG45901	Arabidopsis thalia
34	571	39.6	273	21 AAG23832	Arabidopsis thalia
35	571	39.6	273	21 AAG45900	Arabidopsis thalia
36	567	39.3	196	21 AAB19092	Protein encoded by
37	561	38.9	194	19 AAB46775	Amino acid sequenc
38	557	38.7	266	21 AAG08191	Arabidopsis thalia
39	550.5	38.2	187	19 AAM62792	Trypanoxin perox
40	513.5	35.6	147	21 AAG01615	Human secreted pro
41	507	35.2	224	23 ABB77458	Fungal stress respo
42	491	34.1	263	15 AAB63754	New flower bud ind
43	462	32.1	202	21 AAB13474	Protein encoded by
44	462	32.1	202	22 AAG83150	Protein encoded by
45	462	32.1	202	23 ABB94121	Chlamydia protein

## ALIGNMENTS

XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
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PT DNA encoding human natural killer cell enhancing factor C - useful  
 PT for preventing or treating viral infections, inflammation, neoplasia  
 PT and damage from superoxide radicals  
 PS  
 PS Claim 1; Fig 1; 61pp; English.

CC This sequence represents the human natural killer cell enhancing factor  
 CC (NKEF) C. Natural killer cells (NK) are a subset of lymphocytes capable  
 CC of lysing a variety of tumour cells without prior activation.  
 CC Lymphokine-activated killer cells (LAK) are mainly NK cells activated by  
 CC interleukin-2, and are capable of lysing wider ranges of tumour cells  
 CC with higher cytotoxic activity. NK/LAK activity is influenced by various  
 CC components of blood, including the NKEF A and B proteins. Transfection of  
 CC NKEF into cells results in cell-type-dependent enhanced cell  
 CC proliferation or growth inhibition. The NKEF proteins are antioxidants,  
 CC but show no sequence homology to other antioxidants, such as catalase or  
 CC superoxide dismutase. This sequence, or the DNA encoding it can be used  
 CC to inhibit the cytopathic effect of vesicular stomatitis virus and to  
 CC inhibit the growth of leukaemia cells, or to treat a patient in need of a  
 CC NKEF C polypeptide. Disease or susceptibility to disease related to an  
 CC under-expression of this protein can be diagnosed by determining a  
 CC mutation in the DNA encoding this sequence. This protein can also be used  
 CC to identify compounds which bind to and activate a receptor for it. The  
 CC products can also be used to treat viral infections, inflammation,  
 CC neoplasia and damage from superoxide radicals.

CC  
 CC Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 18; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-147;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGMETERRPRTRRECHFFVAGGOVY 60  
 DB 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGMETERRPRTRRECHFFVAGGOVY 60  
 QY 61 PGEASRVSVADHSHLSKAKISKAPAYWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120  
 DB 61 PGEASRVSVADHSHLSKAKISKAPAYWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120  
 QY 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDL 180  
 DB 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDL 180  
 QY 181 THQISKDYGVYLEDSGHTLRGLFTIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 DB 181 THQISKDYGVYLEDSGHTLRGLFTIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLKTFDKLN 271  
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLKTFDKLN 271

RESULT 2

AA433399  
 ID AAY43399 standard; Protein; 271 AA.

AC AAY43399;

DT 28-JAN-2000 (first entry)

DE Human natural killer cell enhancing factor C protein sequence.

KW Natural killer cell enhancing factor C; NKEF C; human; diagnosis; probe;

KM viral infection; inflammation; neoplasia; superoxide radical damage;

OS Homo sapiens.

PN US5985612-A.

PD 16-NOV-1999.

PF 06-JUN-1995; 95US-0467265.  
 XX  
 PR 06-JUN-1995; 95US-0467265.  
 XX

PA (YUGG/) YU G.  
 PA (GENTZ/) GENTZ R.  
 PA (ROSE/) ROSEN C A.  
 PA (NIJ/) NI J.

PI Gentz R, Rosen CA, Yu G, Ni J;

DR WPI: 2000-012791/01.  
 DR N-PSDB: AA237242.

PT Isolated polynucleotides encoding human natural killer cell enhancing  
 PT factor C, useful for preventing, diagnosing or treating viral  
 PT infections, neoplasia and damage from superoxide radicals -  
 PS  
 PS Claim 1; Fig 1; 29pp; English.

CC This sequence is the human natural killer cell enhancing factor C  
 CC (NKEF C) of the invention. NKEF C protein and DNA sequences can be used  
 CC in the diagnosis, prevention and treatment of disorders associated with  
 CC inappropriate expression and activity (normally reduced) of NKEF C and to  
 CC augment the action of natural killer cells and proteins. The NKEF C  
 CC sequences may be used to treat disorders such as viral infections,  
 CC inflammation, neoplasia and damage from superoxide radicals. They may be  
 CC administered to treat the above diseases by rectifying mutations or  
 CC deletions in a patient's genome that affect the activity of NKEF C by  
 CC expressing NKEF C fragments or to supplement the patients own production  
 CC of NKEF C. Antisense nucleic acid molecules may be administered to down  
 CC regulate NKEF C expression by binding with the cells own NKEF C genes and  
 CC preventing their expression. The NKEF C DNA and antisense molecules may  
 CC also be used as probes in diagnostic assays to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples, and hence which  
 CC patients may be in need of restorative therapy. They may also be used to  
 CC study the expression and function of NKEF C and its role in metabolism.  
 CC NKEF C fragments may be used as antigens in the production of antibodies  
 CC against NKEF C and in assays to identify modulators (agonists and  
 CC antagonists) of NKEF C expression and activity. Anti-NKEF C antibodies  
 CC and NKEF C antagonists may also be used to down regulate NKEF C  
 CC expression and activity. They may be used in this way to treat disorders  
 CC such as the treatment of bone marrow rejection. The antibodies may also  
 CC be used as diagnostic reagents for identifying the presence of NKEF C in  
 CC samples.

CC  
 CC Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-147;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGMETERRPRTRRECHFFVAGGOVY 60  
 DB 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGMETERRPRTRRECHFFVAGGOVY 60  
 QY 61 PGEASRVSVADHSHLSKAKISKAPAYWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120  
 DB 61 PGEASRVSVADHSHLSKAKISKAPAYWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120  
 QY 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDL 180  
 DB 121 TFVCPTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDL 180  
 QY 181 THQISKDYGVYLEDSGHTLRGLFTIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 DB 181 THQISKDYGVYLEDSGHTLRGLFTIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLKTFDKLN 271  
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLKTFDKLN 271

```
RESULT 3
AAM50249
ID AAM50249 standard; Protein; 271 AA.
XX
AC AAM50249;
XX
DT 21-JAN-2002 (first entry)
XX
DE Human natural killer cell enhancing factor C.
XX
KM Natural killer cell enhancing factor C; NKEF C; human; antiviral;
KM virucide; antiinflammatory; cytostatic; antioxidant; vulnerary;
KM therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT /label= Signal_peptide
FT 1..30
FT Protein
FT 31..271
FT /label= Mature_protein
XX
PN US6294164-B1.
XX
PD 25-SEP-2001.
XX
PF 29-SEP-1999; 99US-0407891.
XX
PR 06-JUN-1995; 95US-0467265.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI NI J, Yu G, Gentz R, Rosen CA;
XX
DR WPI: 2001-647258/74.
DR N-PSDB: AAI70524.
XX
PT Natural killer cell enhancing factor C polypeptides encoded by the cDNA
PT in ATCC Deposit No. 97157, useful for preventing or treating viral
PT infections, inflammation, neoplasia or damage from superoxide radicals,
PT e.g. tissue injury -
XX
PS Claim 1; Fig 1; 29pp; English.
XX
CC The present sequence is that of human natural killer cell enhancing
CC factor C (NKEF C), as deduced from a cDNA clone (see AAI70524)
CC isolated from a cDNA library derived from cyclohexamide-treated
CC CEM cells. NKEF C is structurally related to highly conserved
CC oxidative stress proteins and shows 68% identity and 83% similarity
CC to NKEF B. NKEF C is highly expressed in heart, liver, skeletal
CC muscle, pancreas, testis and ovary, moderately expressed in
CC placenta, lung, prostate, small intestine and colon, and lowly
CC expressed in brain, spleen, thymus and peripheral blood leucocytes.
CC NKEF C polypeptide is useful for preventing and/or treating viral
CC infections, inflammation, neoplasia or damage from superoxide
CC radicals (e.g. tissue injury or ageing). The polypeptide may also
CC be used for inhibiting the cytopathic effect of vesicular stomatitis
CC virus and for inhibiting the growth of leukaemia cells. The
CC polypeptide and polynucleotide are also useful as research reagents,
CC for constructing DNA vectors, and for developing therapeutics and
CC diagnostics for treating human disease. Polypeptide fragments of
CC NKEF C that have growth inhibitory or antiviral activity are
CC claimed.
XX
SQ Sequence 271 AA;
XX
Query Match 100.0%; Score 1441; DB 22; Length 271;
Best Local Similarity 100.0%; Pred No. 1.4e-147;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 61 PGEASRVSYADHSLHLSKAKISKAPYWEATVIDEPEFKLTDYRGKLVFFFPPLDF 120
DB 61 PGEASRVSYADHSLHLSKAKISKAPYWEATVIDEPEFKLTDYRGKLVFFFPPLDF 120
QY 121 TFCVCPTEIIAFGDRLEEFPSINTEVVACSVDSQFTHLAMINPRROGGLGPIRIPLLSDL 180
DB 121 TFCVCPTEIIAFGDRLEEFPSINTEVVACSVDSQFTHLAMINPRROGGLGPIRIPLLSDL 180
QY 181 THOISKDYGYLLEDSCGHTLRGLFIIDDKGLRQITLNDLPVGSVDETLLVQAFQYTDK 240
DB 181 THOISKDYGYLLEDSCGHTLRGLFIIDDKGLRQITLNDLPVGSVDETLLVQAFQYTDK 240
QY 241 HGEVCPAGMKPGSETIIPDPAGKLYEDKLN 271
DB 241 HGEVCPAGMKPGSETIIPDPAGKLYEDKLN 271

RESULT 4
AAB82478
ID AAB82478 standard; Protein; 271 AA.
XX
AC AAB82478;
XX
DT 22-AUG-2001 (first entry)
XX
DE Natural killer cell enhancing factor C.
XX
KM Natural killer cell enhancing factor C; NKEF C; human; antioxidant;
KM vulnerary; antiinflammatory; virucide; antitumour; therapy;
KM diagnosis.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT 1..30
FT /label= Signal_peptide
FT 31..271
FT Protein
FT /label= Mature_protein
XX
PN US625079-B1.
XX
PD 03-JUL-2001.
XX
PF 06-JUN-1995; 95US-0467265.
XX
PR 06-JUN-1995; 95US-0467265.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI NI J, Yu G, Gentz R, Rosen CA;
XX
DR WPI: 2001-396982/42.
DR N-PSDB: AAF90573.
XX
PT Isolated polynucleotides encoding human natural killer cell enhancing
PT factor C, useful for preventing, diagnosing or treating viral
PT infections, neoplasia and damage from superoxide radicals -
XX
PS Claim 1; Fig 1; 49pp; English.
XX
CC The present sequence is that of human natural killer cell enhancing
CC factor C (NKEF C). NKEF C is highly expressed in heart, liver,
CC skeletal muscle, pancreas, testis and ovary, moderately in
CC placenta, lung, prostate, small intestine and colon, and lowly
CC expressed in brain, spleen, thymus and peripheral blood
CC leucocytes. cDNA (see AAF90573) encoding NKEF C was derived from
CC cyclohexamide-treated CEM cells. The protein shows 83.3% amino
CC acid similarity to NKEF B, and shows significant homology to several
CC other proteins (thiol-specific antioxidants) from a wide range of
CC organisms. The invention provides NKEF C polypeptides, especially
CC a polypeptide comprising amino acids 1-271, 2-271 or 31-271 of the
CC present sequence, isolated nucleic acids encoding them, and methods
```

CC of producing the polypeptides in recombinant host cells. The NKEF  
 CC C polypeptides and polynucleotides can be used to inhibit the  
 CC growth of leukemia cells, to treat viral infection, to augment the  
 CC effects of NK protein, to treat neoplasias such as tumours and  
 CC cancers, to prevent inflammation, and to prevent damage from  
 CC superoxide radicals in the body e.g. in tissue injury and ageing.  
 CC The polypeptides can also be used to screen for potential agonists  
 CC and antagonists of NKEF C activity. Antagonists may be useful in  
 CC the treatment of bone marrow transplant rejection.

SO Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 22; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60  
 DB 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60  
 QY 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120  
 DB 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120  
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDQFTHLAMINTPRQGLGPIRIPLSDL 180  
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDQFTHLAMINTPRQGLGPIRIPLSDL 180  
 QY 181 THOISKDGYVLEDSGHTLGLFTIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 DB 181 THOISKDGYVLEDSGHTLGLFTIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271  
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

#### RESULT 5

ABB68038  
 ID AAB68038 standard; peptide; 271 AA.

AC AAB68038;

DT 29-JUN-2001 (first entry)

DE Amino acid sequence of the acid form of peroxylredoxin TXN.

KW Peroxylredoxin; acid form; oxidative stress; cell death; cancer;

KW autoimmune disease; neurodegeneration; metabolic disorder.

OS Homo sapiens.

PN FR2798672-A1.

PD 23-MAR-2001.

PF 17-SEP-1999; 99FR-0011663.

PR 17-SEP-1999; 99FR-0011663.

PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PI Rab11Loud T;

DR WPI: 2001-259869/27.

Purified acid form of peroxylredoxin, a marker of oxidative stress,  
 useful in diagnosis and for identifying potential apoptotic and  
 anti-apoptotic agents comprises a specific amino acid motif close to  
 the active site -

Claim 12; Page 23-24; 28pp; French.

CC The present sequence represents the acid form of a human peroxylredoxin  
 CC enzyme. The acid form of peroxylredoxin is a characteristic marker of  
 CC oxidative stress that can be measured simply and quickly, providing a  
 CC reliable indication of stress even where this is of short duration.  
 CC Modulators of the acid form of peroxylredoxin enzyme are used for the  
 CC stimulation or inhibition of apoptosis. Compounds that stimulate  
 CC formation of the acid form of peroxylredoxin are used to induce cell  
 CC death (treatment of cancer and autoimmune diseases) while those that  
 CC inhibit its formation are used to prevent cell death (treatment of  
 CC neurodegeneration). Measuring the ratio between acid form and the native  
 CC form of peroxylredoxin is used to diagnose metabolic disorders associated  
 CC with oxidative stress.

SO Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 22; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60  
 DB 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60  
 QY 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120  
 DB 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120  
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDQFTHLAMINTPRQGLGPIRIPLSDL 180  
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDQFTHLAMINTPRQGLGPIRIPLSDL 180  
 QY 181 THOISKDGYVLEDSGHTLGLFTIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 DB 181 THOISKDGYVLEDSGHTLGLFTIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271  
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

#### RESULT 6

ABB57947  
 ID ABB57947 standard; Protein; 242 AA.

AC ABB57947;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide seq ID NO 633.

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS Drosophila melanogaster.

PN MO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL02050.

New isolated nucleic acid detection reagent for detecting 1000 or more  
 genes from Drosophila and for elucidating cell signalling and cell-cell



PT Interactions -  
 XX  
 XX  
 PS Disclosure; SEQ ID NO 633; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB13511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB572072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 CC  
 XX  
 SO Sequence 242 AA:  
 Query Match 59.3%; Score 854.5; DB 22; Length 242;  
 Best Local Similarity 65.2%; Pred. No. 4,5e-84;  
 Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;  
 Oy 25 LILFLPAGAVOGWTEPRPRRECHHPYAGGVYPCGASRVADHSLHLSKAKISKP 84  
 Db 5 LSVLLSALVGAAPED----NESCYSFAGSVYDPQPK----GDHQLQYTKAVISKP 55  
 Oy 85 APWEGTAVIOGEFKEKLTDYRGKYLVEFFPLDFTVPCPEIIAFGRLEEFSSINTE 144  
 Db 56 APQEGTAVVKEIYKLSISQYLGKIVVLLPDLFTVPCPEIIAFGRLEEFSSINTE 115  
 Oy 145 VVACVSQDFHTLAMIINPRROGGLGPIRIPLLSDLTHQISKDYGVYEDSGHTRGLEFI 204  
 Db 116 VIGVSVDSHFHTLAMIINPRKREGGLGDKIPILSLDTHKISDGVYLESSGHALRGLEFI 175  
 Oy 205 IDDKILQIOTINDLPVGRSVDETRLVQAFQYTRKHGECVCPAGKPGSETIIPRAGKL 264  
 Db 176 IDQGTGLQIOTINDLPVGRSVDETIRLVQAFQYTRKHGECVCPAGKPGADITVPPEEXT 235  
 Oy 265 KYFDKLN 271  
 Db 236 KYFAKNN 242  
 RESULT 7  
 AAB43528 standard; Protein: 233 AA.  
 ID AAB43528;  
 AC AAB43528;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE Human cancer associated protein sequence SEQ ID NO:973.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiyiral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05882.  
 XX  
 PR 12-MAR-1999; 99US-0124270.

XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI: 2000-587533/55.  
 XX  
 DR N-PSDB: AAC77737.  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer -  
 XX  
 PS Claim 11; Page 1542-1543; 2352pp; English.  
 CC AAC7607 to AAC78448 encode the human cancer associated proteins given  
 CC in AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnary; immunomodulator;  
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention.  
 XX  
 SO Sequence 233 AA:  
 Query Match 52.1%; Score 750.5; DB 21; Length 233;  
 Best Local Similarity 67.1%; Pred. No. 8e-73;  
 Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;  
 Oy 64 ASRVSVADHSLHLSKAKISKPAPWEGTAVI-DGEFEKELTDYRGKYLVEFFPLDFTF 122  
 Db 25 ATCVGTADRKMSGNAKIGHAPAPNFKATAVMDGQFQKSLSDYKGVVFFFTYLDFTF 84  
 Oy 123 VCPTEIIAFGRLEEFRRSINTEVACVSQDFHTLAMIINPRROGGLGPIRIPLLSDLTH 182  
 Db 85 VCPTEIIAFSDRAEEFKKLNCOVIGASVDSHFCHLAWVTTPKQGLGPMNIPLVDPKR 144  
 Oy 183 QISKDYGVYLEDSCHTLGLFTIDDKGILROTLNDLPVGRSVDETIRLVQAFQYTRKHG 242  
 Db 145 TTAQDYGVAKADEGISTFQKGLFTIDDKGILROTLNDLPVGRSVDETIRLVQAFQYTRKHG 204  
 Oy 243 EVCAPGAKPGSETIIPDPAGKLKYPDK 269  
 Db 205 EVCAPGAKPGSPTIKRDPVQKSEYFSK 231  
 RESULT 8  
 ABP41353 standard; Protein: 233 AA.  
 ID ABP41353;  
 AC ABP41353;  
 XX  
 DT 23-AUG-2002 (first entry)  
 DE Human ovarian antigen HCOO501, SEQ ID NO:2485.  
 XX  
 DT  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;



[illegible]

RESULT	10
AAB68040	
ID	AAB68040 standard; peptide; 198 AA.
XX	
AC	AAB68040;
XX	
DT	29-JUN-2001 (first entry)
XX	
DE	Amino acid sequence of the acid form of peroxiredoxin TDx2.
XX	
KW	Peroxyredoxin; acid form; oxidative stress; cell death; cancer;
RW	autoimmune disease; neurodegeneration; metabolic disorder.
XX	
OS	Homo sapiens.
XX	
PM	FR2798672-A1.
XX	
PD	23-MAR-2001.
XX	
XX	
PF	17-SEP-1999; 99FR-0011663.
XX	
PR	17-SEP-1999; 99FR-0011663.
XX	
PA	(COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PI Rabillood T:  
 DR  
 XX WPI: 2001-2259869/27.  
 XX  
 PR Purified acid form of peroxylredoxin, a marker of oxidative stress,  
 PR useful in diagnosis and for identifying potential apoptotic and  
 PR anti-apoptotic agents comprises a specific amino acid motif close to  
 PR the active site -  
 XX  
 PS  
 XX  
 Claim 12; Page 25-26; 28pp; French.  
 CC  
 CC The present sequence represents the acid form of a human peroxylredoxin  
 CC enzyme. The acid form of peroxylredoxin is a characteristic marker of  
 CC oxidative stress that can be measured simply and quickly, providing a  
 CC reliable indication of stress even where this is of short duration.  
 CC Modulators of the acid form of peroxylredoxin enzyme are used for the  
 CC stimulation or inhibition of apoptosis. Compounds that stimulate  
 CC formation of the acid form of peroxylredoxins are used to induce cell  
 CC death (treatment of cancer and autoimmune diseases) while those that  
 CC inhibit its formation are used to prevent cell death (treatment of  
 CC neurodegeneration). Measuring the ratio between acid form and the native  
 CC form of peroxylredoxin is used to diagnose metabolic disorders associated  
 CC with oxidative stress.  
 XX  
 Sequence 198 AA:  
 SO

Query Match	50.0%;	Score 721;	DB 22;	Length 198;
Best Local Similarity	69.8%;	Pred. No. 1e-65;		
Matches 134;	Conservative 25;	Mismatches 31;	Indels 2;	Gaps 2
QY 79	AKISRPAPYMEGNAV	-DGEFKELKLTVDYRGKVLVEFP	PLDPTVFCPEITIAFGRLDE	137
	::    :	:    :		
Db 6	AKIGHAPAPNFKA	VAWPDQFNDISDYGKRVWFETPLDPTFCPEITIAFSRAEE		65
QY 138	FISINFEVACVSQ	SQFTLLHMIINPRRQGCIPRI	PLISDLTHQISDXYGLYEDSCH	197
	::: :: ::	:		:
Db 66	FKKLNQVIGASV	SDFHCHLAWNTPKKGGCLPMIPLVSDPKRTIADYGLKRADEI		125
QY 198	TURGLFIIDDKGIL	ROIITINDLTPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII		257

Db	Qy	Db	Qy
126	258	185	269
SFRGFIIDDDGILRQITVNDLVGRSVDETLRL-QAFQETDKHGVECPAGMWRGSDTIK	PDPAGKLTYPDK	PDVOKSKEYFSK	

RESULT	11
AAU78580	
ID	AAU78580 standard; Protein: 198 AA.
XX	
AC	AAU78580;
XX	
DT	05-JUN-2002 (first entry)
XX	
DE	Mouse peroxiredoxin II-1 (PrxII-1) protein.
XX	
KW	Peroxioredoxin; Prx; promoter; PrxII-1.
XX	
OS	Mus sp.
XX	
FH	Key
FT	Misc-difference 7 location/Qualifiers
FT	/note= "Encoded by CAA"
FT	Misc-difference 97
FT	/note= "Encoded by GGC"
XX	
PN	KR99066020-A.

PR 20-JAN-1998; 98KR-0001604.  
XX  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
XX  
PI Yeom YI, Lim MJ, Lee GG, Yoo DY;  
XX  
DR WPI; 2000-547264/50.  
DR N-PDSB; ABK47315.  
XX  
PT Peroxiredoxin PRX II-1 and promoter derived from mouse, base sequence  
PT of PRX II-2 and PRX II-3 -  
XX  
XX  
PS Disclosure; Fig 6; 14pp; English.  
XX  
XX This invention relates to the sequence of the mouse peroxiredoxin  
CC IT-1 (Prxi1-1) promoter. The invention also comprises the cDNA  
CC sequences encoding the mouse Prxi1, Prxi1-2 and Prxi1-3 proteins.  
CC The present sequence represents the mouse peroxiredoxin protein  
CC sequence of the invention.  
XX  
SQ Sequence 198 AA;

	Query Match	Similarity	49.9%	Score 719;	DB 21	length 198;
	Best Local	Similarity	68.9%	Pred. No. 1.7e-69;		
	Matches	133;	Conservative	22;	Mismatches	38;
					Indels	0;
					Gaps	0;
QY	79	AKISKPAPWEAGTAVIDGFEKELKLDYNGKGLVFEFFYELDPTFVCPTEIIAFGRLEEF				138
Db	6	AHIGKAPDPETAAYVDGAFKEIKLSDYNGKGVLEFFYELDPTFVCPTEIIAFSDHADEF				65
QY	139	RSINTEVACVSDSOFTHLAMINTPRGGCLGPIRILPLSDLTQIISKDYGYLEDSGHT				198
Db	66	RKIGCEVILSVSDSOFTHLAMINTPRKEGGLPLNPLADVYKLSQVAYGLKNDGEGIA				125
QY	199	LRGLFTIDDKGILROTLNDLPIGRSVDEETLRLVYQFOYTDKHGEVCPAGMKPGSETIIP				258
Db	126	YRGLFTIIDDKGVIRQTLTVNDLPIGRSVDEALRLVYQFOYTDDEHGEVCPAGMKPGSPNINIP				185
QY	259	DPAGKLTKEFDKLN				271



## RESULT 14

ID AAM09793 standard; Protein: 199 AA.

XX AAM09793;

XX 10-JUN-1997 (first entry)

XX Natural killer cell enhancing factor A.

XX NKEF-A; NKEF-B; natural killer cell enhancing factor; protect;

XX mixed metal-thiol oxidative inactivation; increase activity;

XX enhancement; stimulate; interleukin-2; IL-2; lymphocyte activation;

XX proliferation; combined immunotherapy; cytokine.

XX Homo sapiens.

XX US5610286-A.

XX 11-MAR-1997.

XX 04-NOV-1991;

XX 31-AUG-1994; 94US-0299162.

XX 04-NOV-1991; 91US-0787148.

XX 03-MAY-1994; 94US-0232189.

XX (REGC ) UNIV CALIFORNIA.

XX Golub SH, Shau H;

XX WPI: 1997-178453/16.

XX N-PSDB: AAT62696.

XX Claim 1; Column 21-24; 18pp; English.

XX AAM09793-94 are the amino acid sequences for natural killer cell

XX enhancing factors (NKEF A and B respectively. The DNA (AAT62696-97)

XX encoding them is useful for prodn. of recombinant NKEF A and B, which may

XX have the same biological activities as native NKEF. Native NKEF protects

XX enzymes from mixed metal-thiol oxidative inactivation and increases the

XX activity of NK cells when used alone or in combinations with other NK

XX cell enhancement proteins, e.g. interleukin (IL) 2. It is useful in

XX in-vivo and in-vitro applications where it is desirable to stimulate NK

XX cell activity and is effective with IL-2 in inducing lymphocyte

XX activation and proliferation and thus may be used for combined

XX immunotherapy with cytokines, e.g. IL-2, TNF or interferon, to increase

XX the function of B cells, T cells, macrophages, NK cells and other

XX leukocytes.

XX Sequence 199 AA;

XX SQ

Query Match 49.5%; Score 713.5; DB 18; Length 199;

Best Local Similarity 68.8%; Pred. No. 6-6e-69;

Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISRPAPYWGEGTAVI-DGEFKELITDYGKYLVEFFYPDLDTFVCPTEIIAFGDRLEE 137

DB 6 AKIGHAPAPMFKAATAVWDQFKDISLDYKGYVFFFPDLFTFVCPTEIIAIFSRAEE 65

QY 138 FESINTEVACVDSQFHTLAMIINPRROGGIGPIRIPLISDLTHOISDYGVLDSGH 197

DB 66 FKLKLCQVIGASVDSHFCLAWNPVKOGGLGPMNIPVSPKRTIADYGLKADDECI 125

QY 198 TARGLEIIDDKGLIROLITNDLPVGRSVDETLRLVQAFQYTDKRGEGVCPAGMPCSEETII 257

DB 126 SFRGLFTIIDDKGLIROLITVNDPFCRSVDETLRLVQAFQYTDKRGEGVCPAGMPCSEETII 185

## RESULT 15

ID AAB56959 standard; Protein: 224 AA.

XX AAB56959;

XX 13-MAR-2001 (first entry)

XX Human prostate cancer antigen protein sequence SEQ ID NO:1537.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;

XX neuroprotective; cytostatic; cardioprotective; immunomodulatory; muscular;

XX vulnery; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;

XX antibacterial; gene therapy; neural; immune; reproductive; renal;

XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;

XX wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000MO-US05988.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI: 2000-587513/55.

XX N-PSDB: AAF16162.

XX Prostate cancer associated gene sequences, referred to as prostate

XX cancer antigens, useful for treatment, prevention, and diagnosis of

XX disorders such as prostate cancer -

XX Claim 11; Page 1979; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated

XX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

XX The prostate cancer antigens can have neuroprotective, cytostatic,

XX cardioprotective, immunomodulatory, muscular, vulnery, gastrointestinal,

XX nephrotoxic, antineoplastic, gynaecological and antibacterial activities,

XX and can be used in gene therapy. The prostate cancer antigen

XX polynucleotides may be used for detection of prostate cancer. Chromosome

XX identification, as chromosome markers, and for numerous other diagnostic

XX or research purposes. The prostate cancer antigens may be used to treat

XX disorders such as neural, immune, muscular, reproductive,

XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

XX disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to

XX AAB57303 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 224 AA;

XX SQ

Query Match 48.8%; Score 703; DB 21; Length 224;

Best Local Similarity 66.5%; Pred. No. 1.1e-67;

Matches 127; Conservative 28; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAPYWGEGTAVI-DGEFKELITDYGKYLVEFFYPDLDTFVCPTEIIAFGDRLEERS 140

DB 33 VYQHARYFGTAVVNEDEFSLDDEKRGKYLVEFFYPDLDTFVCPTEIIAIFSRAEFPID 92

QY 141 INTEVACVDSQFHTLAMIINPRROGGIGPIRIPLISDLTHOISDYGVLDSGH 200

Db 93 VNCVVAVSVDSHFSHLAMINTPRKNGGIGHMNTALLSDLTKOISRQYGVLEGGSLAR 152  
OY 201 GLFIIDDKGILROITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGWPGSEIIPDP 260  
Db 153 GLFIIDPNCVIRKHLNVNDLPVGRSVETLRLVKAFOYVETHGGEVCPANWTPDSPTIKPS 212  
OY 261 AGKLKTFEDKLN 271  
Db 213 AASKEYFOKVN 223

Search completed: January 17, 2003, 19:18:23  
Job time : 41 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:16:47 : Search time 35 Seconds  
(without alignments)  
1595.393 Million cell updates/sec

Title: US-09-911-346-2  
Perfect score: 1441  
Sequence: 1 MEALPLLAATPDHGRHRL.....GSETIIPDPKLYEDKLN 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21: \*  
1: sp.archaea: \*  
2: sp.bacteria: \*  
3: sp.fungi: \*  
4: sp.human: \*  
5: sp.invertebrate: \*  
6: sp.mammal: \*  
7: sp.mhc: \*  
8: sp.organelle: \*  
9: sp.phage: \*  
10: sp.plant: \*  
11: sp.rodent: \*  
12: sp.virus: \*  
13: sp.vertebrate: \*  
14: sp.unclassified: \*  
15: sp.virus: \*  
16: sp.bacteriaph: \*  
17: sp.archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1296	89.9	274	6	Q9BG12
2	1266.5	87.9	273	11	Q9ZOV5
3	877	60.9	223	5	Q9BIF6
4	854.5	59.3	242	5	Q9V304
5	749	52.0	199	6	Q9BG13
6	734	50.9	199	5	Q9Y082
7	733	50.9	198	11	Q9CWJ4
8	727	50.5	198	11	Q9B376
9	723.5	50.2	199	11	Q9JKY1
10	721.5	50.1	199	6	Q9BG14
11	721.5	50.1	199	13	Q93241
12	721	50.0	195	5	Q9N198
13	718.5	49.9	199	11	Q9CW12
14	718	49.8	198	11	Q9DB49
15	717	49.8	196	5	Q8W5F6
16	715	49.6	194	5	Q9V3P0

17	708	49.1	193	5	Q8WQ02
18	702.5	48.8	199	13	Q91886
19	701	48.6	576	5	Q19265
20	695	48.2	199	5	Q76452
21	695	48.2	247	5	Q8T4L6
22	688	47.7	199	5	Q44941
23	683	47.4	199	5	Q16026
24	679	47.1	199	5	Q44366
25	678	47.1	199	5	Q9G0B2
26	676	46.9	199	5	Q16006
27	676	46.9	257	11	Q9ZOV6
28	673.5	46.7	219	5	Q9GNF6
29	654.5	45.4	193	5	Q8TC64
30	650	45.1	220	5	Q9VEJ0
31	650	45.1	224	5	Q9GPO3
32	647.5	44.9	185	5	Q96380
33	642	44.6	226	5	Q9G047
34	640	44.4	226	5	Q79469
35	634	44.0	192	3	Q74887
36	629	43.7	185	5	Q97161
37	617.5	42.9	226	5	Q95089
38	614.5	42.6	226	5	Q9U1B5
39	613.5	42.6	235	10	Q9FE86
40	609.5	42.3	199	5	Q96763
41	605	42.0	199	10	Q9FNS2
42	595.5	41.3	199	5	Q8W5H1
43	594	41.2	194	5	Q9Y0D3
44	591	41.0	199	5	Q9T6S4
45	588.5	40.8	203	16	Q8VNC5

#### ALIGNMENTS

RESULT 1	ID	Q9BG12	PRELIMINARY	PRT	274 AA.
AC	Q9BG12				
DT	01-JUN-2001 (TREMURel. 17, Created)				
DT	01-JUN-2001 (TREMURel. 17, Last sequence update)				
DT	01-DEC-2001 (TREMURel. 19, Last annotation update)				
DE	Peroxioredoxin 4.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RA	TISSUE=LIVER;				
RA	Leyens G., Donnay I., Knoops B.;				
RT	"Cloning of a new bovine peroxiredoxin, and screening of the complete				
RT	peroxiredoxin family in different bovine tissues.";				
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF05563; AAG53660.1; -				
DR	HSSP: P30041; 1PRX.				
DR	InterPro: IPR000866; Ahpc-TSA.				
DR	Pfam: PF00578; Ahpc-TSA; 1.				
SQ	SEQUENCE 274 AA; 30741 MW; AE1416CFC170E37 CRC64;				
Query Match	89.9%	Score 1296:	DB 6:	Length 274:	
Best Local Similarity	92.1%	Pred. No. 2.7e-116:			
Matches 246:	Conservative	8:	Mismatches 13:	Indels 0:	Gaps 0:
QY	5	PLLAATPDHGRHRLLLPLLLFLPAGAVQGVETEERTREECHEFYAGGVYGOEA	64		
QY	1				
Db	8	PLPLATPLAPGRSKLLPLLEFLFLRAEAVRGFEAREPRTRRECHFFYAGGVYGEV	67		
QY	65	SRVSVADSHLSLAKISKAPYWEAGTAVIDGEFKEKLTDYRGKYLVEFFYPIDFTFVC	124		
QY	1				
Db	68	SRVSVADSHLSLAKISKAPYWEAGTAVIDGEFKEKLTDYRGKYLVEFFYPIDFTFVC	127		
QY	125	PTELIAGDRLEFRFRSINTEVVACVDSQFTHLAMWTPRNGGLGRIRPLLSDLTHQI	184		

Db 128 PREIIIAFGRIIDEFIRINTEVACSVDSQFTHLAMINTPRROGGLSINIMPLIADLNHOI 187  
 OY 185 SKDGYVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGEV 244  
 Db 188 SKDGYVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGEV 247  
 OY 245 CPAGMKPGSETIIPDPACKLKFKYFDKLN 271  
 Db 248 CPAGMKPGSETIIPDPACKLKFKYFDKLN 274

## RESULT 2

O920V5 PRELIMINARY: PRT: 273 AA.  
 AC O920V5;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PRX IV.  
 CN PRX IV.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99148808; Pubmed=10025941;  
 RA Matsuno A., Okado A., Fujii T., Fujii J., Egashira M., Mikawa N.,  
 RA Taniguchi N.,  
 RT "Cloning of the peroxiredoxin gene family in rats and characterization  
 of the fourth member."  
 RL FEBS Lett. 443:246-250(1999).  
 DR EMBL; AF106945; AAD17993.1; -  
 DR HSSP; P30041; 1PRX.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 SQ SEQUENCE 273 AA; 31007 MW; 09E614794F1DC6C2 CRC64;

Query Match 87.9%; Score 1266.5; DB 11; Length 273;  
 Best Local Similarity 90.3%; Pred. No. 1.8e-113;  
 Matches 242; Conservative 10; Mismatches 13; Indels 3; Gaps 2;

OY 6 LLAATPDHGRHRLLL--PLLEFLPAGAVQGETEERPRTRRECHYAGGVYRGE 63  
 Db 7 LLLGTPPSR-RMKRLVLLPLPLFLQLQTEALGLESDDFRFRNENCHYAGGVYRGE 65  
 OY 64 ASRVSVADHSLHLSKATISKRPARYWESTAVIDGFEKELTDYRGKLVFFFPDLDFEV 123  
 Db 66 VSRVSVADHSLHLSKATISKRPARYWESTAVINGEFKELTDYRGKLVFFFPDLDFEV 125  
 OY 124 CPTEIIAFCGRLEEFPSINTEVACSVDSQFTHLAMINTPRROGGLSINIMPLIADLNHOI 185  
 Db 126 CPTEIIAFCGRLEEFPSINTEVACSVDSQFTHLAMINTPRROGGLSINIMPLIADLNHOI 185  
 OY 184 ISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGE 243  
 Db 186 ISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGE 245  
 OY 244 VCPAGMKPGSETIIPDPACKLKFKYFDKLN 271  
 Db 246 VCPAGMKPGSETIIPDPACKLKFKYFDKLN 273

## RESULT 3

O9BIF6 PRELIMINARY: PRT: 223 AA.  
 AC O9BIF6;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Thioresdoxin peroxidase Bgtrp (Fragment).  
 OS Biomphalaria glabrata (Bloodfluke planorb).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Planorbidae; Biomphalaria.  
 OX NCBI\_TaxID=6526;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LAC; TISSUE=ALBUMEN GLAND;  
 RA Cousin C., Ofori K., Okulate M., Grant J., Richards C., Lewis F.,  
 RA Knight M.,  
 RT "Biomphalaria glabrata: Molecular differences between the albumen  
 RT glands of susceptible and non-susceptible snails."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY026258; AAK26236.1; -  
 DR HSSP; P30041; 1PRX.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 DE Peroxidase.  
 FT NON\_TER  
 SQ SEQUENCE 223 AA; 25033 MW; B5B995442C1BP906 CRC64;

Query Match 60.9%; Score 877; DB 5; Length 223;  
 Best Local Similarity 76.5%; Pred. No. 3.7e-76;  
 Matches 163; Conservative 18; Mismatches 30; Indels 2; Gaps 1;

OY 55 AGGOVYVGEASVADSHLSKATISKRPARYWESTAVIDGFEKELTDYRGKLVFF 114  
 Db 5 AGGOVYVGEASVADSHLSKATISKRPARYWESTAVIDGFEKELTDYRGKLVFF 62  
 OY 115 FYPLDFVFCPTTEIIAFCGRLEEFPSINTEVACSVDSQFTHLAMINTPRROGGLSINIMPLIADLNHOI 174  
 Db 63 FYPLDFVFCPTTEIIAFCGRLEEFPSINTEVACSVDSQFTHLAMINTPRROGGLSINIMPLIADLNHOI 122  
 OY 175 PLSLDLHQISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGEV 234  
 Db 123 PLSLDLHQISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRLVNAFOYTDKHGEV 182  
 OY 235 FOYTDKHGEVCPAGMKPGSETIIPDPACKLKFKYFDKLN 267  
 Db 183 FOYTDKHGEVCPAGMKPGSETIIPDPACKLKFKYFDKLN 215

## RESULT 4

O9V304 PRELIMINARY: PRT: 242 AA.  
 AC O9V304;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CG1274 protein (SECRETABLE thioredoxin peroxidase) (GH25379P).  
 GN JAFRAC2 OR CG1274.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; Pubmed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Balowin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.D., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,



RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideguchi C.,  
RA Jaleli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclob J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissensbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20098524; PubMed-10632718;  
RA Rodriguez J., Agudo M., Van Damme J., Vandekerckhove J.,  
RA Santaren J.F.,  
RT "Polypeptides differentially expressed in imaginal discs define the  
RT peroxiredoxin family of genes in *Drosophila*.";  
RL Eur. J. Biochem. 267:487-497(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Radvuk S.N., Spinola B., Klichko V.I., Orr W.C.,  
RT "Cloning, expression and characterization of the peroxiredoxin gene  
RT family in *Drosophila melanogaster*.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RA Stapleton M., Brokslein P., Hong L., Abhayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuncio J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AEO03476; AAF47704.1; -;  
DR EMBL: AF167099; AAF42986.1; -;  
DR EMBL: AF321614; AAK06769.1; -;  
DR EMBL: AY060785; AAL28333.1; -;  
DR FLYBase; FBgn0040308; Jafnac2.  
DR InterPro: IPR000866; Ahpc-TSA.  
DR Pfam; PF00578; Ahpc-TSA; 1.  
KW Peroxidase.  
SQ SEQUENCE 242 AA; 26743 MW; 8A0142FB19D9564 CRC64;

Query Match 59.3%; Score 854.5; DB 5; Length 242;  
Best Local Similarity 65.2%; Pred. No. 6.1e-74;  
Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;

QY 25 LLLFLPAGVAVGMEETPRPTREECHEHYAGGVYGPGEASVYADSLHLSKAKISKP 84  
DB 5 LSVLLASALVGAKPED-----NESCYSFAGSGVYPPQPK-----GDHQLQYTKAVISKP 55  
QY 85 APYMEGTAVIDGEFKELKLTIDYRGKYLVFFYPPLDFTVPCPTETIAFSDRLSEFSINTE 144  
DB 56 APQEGTAIVNKEIKYLSQYLGKYVVLFFPLDFTVPCPTETIAFSDRLSEFSINTE 115  
QY 145 VVACSVDSQFTHLAINTPRROGGIGPIRIPILSLTHQISKDYVYLEDSSHITRGIFI 204  
DB 116 VIGVSVDSHFTHLAINTPRREGGIGDKVPIPLSLDTHKISKDYVYLEDSSHITRGIFI 175  
QY 205 IDDKILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPKPSETIIPPAKGL 264

DB 176 IDQTCVLRQITLNDLPVGRSVDETLRLVQAFQYTDHGEVCPAGKPKPSETIIPPAKGL 235  
QY 265 KYFDKLN 271  
DB 236 KYFAKN 242  
RESULT 5  
QYBG13 PRELIMINARY; PRT; 199 AA.  
AC QYBG13;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
DE Peroxiredoxin 2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-LIVER;  
RA Leyens G., Donnay I., Knoops B.,  
RT "Cloning of a new bovine peroxiredoxins, and screening of the complete  
RT peroxiredoxin family in different bovine tissues.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF305562; AAC53659.1; -;  
DR HSSP; P30041; IPRX.  
DR InterPro: IPR000866; Ahpc-TSA.  
DR Pfam; PF00578; Ahpc-TSA; 1.  
SQ SEQUENCE 199 AA; 21946 MW; 5F256CE54090E2DE CRC64;  
Query Match 52.0%; Score 749; DB 6; Length 199;  
Best Local Similarity 69.1%; Pred. No. 6.4e-64;  
Matches 134; Conservative 26; Mismatches 34; Indels 0; Gaps 0;  
QY 78 KAKISKPAPEYMEGTAVIDGEFKELKLTIDYRGKYLVFFYPPLDFTVPCPTETIAFSDRLSE 137  
DB 6 KAHVGPAPPECATVAVGVAGFEKVLSDYKGYVVLFFYPPLDFTVPCPTETIAFSDRAAE 65  
QY 138 FRSINTEVAVSVDSEFTHLAINTPRROGGIGPIRIPILSLTHQISKDYVYLEDSSGH 197  
DB 66 FHLKCEVGVASVDSQFTHLAINTPRREGGIGPIRIPILSLTHQISKDYVYLEDSSGH 125  
QY 198 TLRLGLFIIDDKGILRLQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPKPSETI 257  
DB 126 AYRGFLVIDKGVLRQVITINDLPVGRSVDEALRLVQAFQYTDHGEVCPAGKPKPSETI 185  
QY 258 PDPAGKLYFDKLN 271  
DB 186 PNVDSKKEFYSKHN 199  
RESULT 6  
QY082 PRELIMINARY; PRT; 199 AA.  
AC QY082;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
DE Peroxiredoxin.  
GN TPX-1.  
OS Globodera rostochiensis (Golden nematode).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.  
OX NCBI\_TaxID=31243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ROL;  
RX MEDLINE-20542028; PubMed-11087915;  
RA Robertson L., Robertson W.M., Sobczak M., Helder J., Tetaud E.,

Query Match	50.9%	Score 734	DB 5	Length 199
Best Local Similarity	67.4%	Pred. No. 1.8e-62		
Matches 130	Conservative 30	Mismatches 33	Indels 0	Gaps 0
RA	Arizanyan M.R., Ferguson M.A.J., Fairlamb A., Jones J.T.;			
RT	"Cloning, expression and functional characterization of a			
RT	peroxiredoxin from the potato cyst nematode <i>Globodera rostochiensis</i> ."			
RL	Mol. Biochem. Parasitol. 111:41-49(2000).			
DR	EMBL: AJ243736; CAB48391.1; -			
DR	HSSP: P30041; 1PRX.			
DR	InterPro: IPR000865; Ahpc-TSA.			
DR	Pfam: PF00578; Ahpc-TSA; 1.			
SO	SEQUENCE 199 AA: 22317 MW: 90AD8274672B0F53 CRC64;			
QY	77	SKAKSRPAPWEGTAVIDGEFEKELKLTDRGKRYLFFFPYPLDFFVCPTEIIAQRDLR	136	
DB	5	SAFKIKPAPKPSADAVNGVNGDEFTISLDYDKGKYVLFPPYDFFVCPTEIIAASDRAD	64	
QY	137	EPFASITVEVAVSDFHFLAMINPPROGGLGPRIPLESDLTHQISKDYGVLEDSG	196	
DB	65	ERRKIDTQILACSTOSKFSHLEIMPKRKGIGEMKIPVLADTHNKSISRDYGVLMEEAG	124	
QY	197	HTLRGLFIIDDKGILRQTLNLDLPVGRSVDEFRLRVLQAFQYDKDKGCVPAKWRGSEI	256	
DB	125	IAFRGLFIIDDKGILRQTLNLDLPVGRSVDEFRLRVLQAFQYDKDKGCVPAKWRGSEI	184	
QY	257	IPDPAGKRLKYPDK 269		
DB	185	KDPESGQTFEFGK 197		
RESULT 7				
Q9CWMJ4	PRELIMINARY;	PRT: 198 AA.		
AC	Q9CWMJ4;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Peroxiredoxin 2.			
GN	PRDX2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;			
RC	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Altawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Resukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Boffelli D., Bojunga N., Carlini P., de Bonaudo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Guinacchioni S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Matchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Notrdone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Yuzhakov-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
DR	EMBL: AK010653; BAB27093.1; -			
DR	HSSP: P30041; 1PRX.			
DR	MGI:109486; Prdx2.			
DR	InterPro: IPR000866; Ahpc-TSA.			
DR	Pfam: PF00578; Ahpc-TSA; 1.			

SQ	SEQUENCE	198 AA;	21811 MW;	819P9DD077A70259 CRC64;
	Query Match	50.9%;	Score 733;	DB 11; Length 198;
	Best Local Similarity	69.9%;	Pred. No. 2, 2e-62;	
	Matches 135;	Conservative 23;	Mismatches 35;	Indels 0; Gaps 0
OY	AKRSKAPVMEGAVAVIDGFEKKELTDYRGKYLVFFFPPLDFTFVCPTETIAGDRLEEF	138		
Dd	AQIGKSAADPETAATVAVDGAFAKEIKLSDRGKVYVLFPPDPDFTEVCPTETIAFSDAEDF	65		
OY	RSINTEVVACVSVDSEPTHLAMINTPRROGGIGPIRIPILSDLTQHQSISDKGVYLEDSGHT	198		
Dd	RKLCEVLGVSVDSQCTHLLAMINTPRKEGGLGPLNIPILDADVTKSLSSONTGVLANDEGIA	125		
OY	LRLGLEFIIDDKGILRQTTLNDLPYGRSVDETLRVLQAFOYTDKHGECVPAGMKPGSETTIP	258		
Dd	YRGLFEIIDAKGVLRQTTVNDELPGVRGSVDALRLVQAFOYTDERHGEVCPAGMKPGSDTIKP	185		
OY	DPAGKCLKYFDKLN	271		
Dd	NVDSKEFYERSKIN	198		
	RESULT 8			
ID	088376 PRELIMINARY; PRT; 198 AA.			
AC	088376			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	Type II peroxiredoxin 1.			
GN	PRDX2 OR PRXII-1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OK	NCBI_Taxid=10090;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=129SVJ.			
RX	MEDLINE=98382588; PubMed=9714804;			
RA	Lim M.T., Chee H.Z., Rhee S.G., Yu D.-Y., Lee K.-K., Yeom Y.I.,			
RT	"rrie type II peroxiredoxin gene family of the mouse: molecular			
RT	structure, expression and evolution.";			
RL	Gene 216:197-205(1998).			
DR	EMBL; AF032722; AAC35744.1; -			
DR	EMBL; AF032718; AAC35744.1; JOINED.			
DR	EMBL; AF032719; AAC35744.1; JOINED.			
DR	EMBL; AF032720; AAC35744.1; JOINED.			
DR	EMBL; AF032721; AAC35744.1; JOINED.			
DR	HSSP; P30041; LPRX.			
DR	MGI; MGI:109486; Prdx2.			
DR	InterPro; IPR000866; Ahpc-TSA.			
DR	Ffam; PF00578; Ahpc-TSA; 1.			
SO	SEQUENCE 198 AA; 21791 MW; EEFB0F5426F717AD CMC64;			
	Query Match	50.5%;	Score 727;	DB 11; Length 198;
	Best Local Similarity	69.4%;	Pred. No. 8, 3e-62;	
	Matches 134;	Conservative 23;	Mismatches 36;	Indels 0; Gaps 0;
OY	AKISKPAVMYGSTVAIOSEFKELTDYRGKYLVFFFPPLDFTFVCPTETIAGDRLEEF	138		
Dd	AQIGKSADPETAATVAVDGAFAKEIKLSDRGKVYVLFPPDPDFTEVCPTETIAFSDAEDF	65		
OY	RSINTEVVACVSVDSEPTHLAMINTPRROGGIGPIRIPILSDLTQHQSISDKGVYLEDSGHT	198		
Dd	RKLCEVLGVSVDSQCTHLLAMINTPRKEGGLGPLNIPILDADVTKSLSSONTGVLANDEGIA	125		
OY	LRLGLEFIIDDKGILRQTTLNDLPYGRSVDETLRVLQAFOYTDKHGECVPAGMKPGSETTIP	258		
Dd	YRGLFEIIDAKGVLRQTTVNDELPGVRGSVDALRLVQAFOYTDERHGEVCPAGMKPGSDTIKP	185		
OY	DPAGKCLKYFDKN	271		
Dd	NVDSKEFYERSKIN	198		

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DB	166	NVDSKEYFSKH	198	
RESULT 9				
DB	09JRY1	PRELIMINARY:	PRT:	199 AA.
AC	09JRY1			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Thioredoxin peroxidase II.			
OS	Cricetus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
CC	Cricetus.			
OX	NCBI_TaxID=10029;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ID 10029;			
RA	Huang R.N., Lee T.C., Chen Y.C., Tam M.F., Chang K.N.;			
RT	"Expression of thioredoxin peroxidase in Chinese hamster ovary			
RT	cells."			
RL	Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF221841; AAF32369.1; -.			
DR	HSSP; P30041; IPRX.			
DR	InterPro; IPR000866; Ahpc-TSA.			
DR	Pfam; PF00578; Ahpc-TSA; 1.			
KW	Peroxidase.			
SO	SEQUENCE 199 AA; 22262 MW; CDA6E8015E1A055E CRC64;			
Query Match 50.2%; Score 723.5; DB 11; Length 199;				
Best Local Similarity 69.8%; Pred. No. 1.8e-61;				
Matches 134; Conservative 25; Mismatches 32; Indels 1; Gaps 1;				
OY	79	AKISRPARYMETATAT-IGEFKEKLTDTYRGKYLVEFFRPDFTVTCPEIIAIFDRLAE	137	
DB	6	AKIGPAPNFATAPWPGQFRDCLSEKRGKVVFFFPDFTVCPTEIIAIFSDRAE	65	
OY	138	FRSITFEVACVDSQFTHLAWINTPRRQGGCIPRIPLSDLTQISKDYGVLDESGH	197	
DB	66	FKKLNCQVIGASVDSHFCHLAWINTPRKQGGCIGPMNIPVSDPKRTIADYGVLADECI	125	
OY	198	TLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVQAFQYTDKNGEYCPAGKPGSEETI	257	
DB	126	SFRGFIIIDDKILRQITLNDLPVGRSVDELRLVQAFQYTDKNGEYCPAGKPGSDRIK	185	
OY	258	PDPAGKLTYPFK 269		
DB	186	PDVOKSEYFSK 197		
RESULT 10				
DB	09BG14	PRELIMINARY:	PRT:	199 AA.
AC	09BG14			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	Peroxiredoxin 1.			
OS	Bos taurus (bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
CC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Leyens G., Donay I., Knoops B.;			
RT	"Cloning of 4 new bovine peroxidoxins, and screening of the complete			
RT	peroxidoxin family in different bovine tissues."			
RL	Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF305561; AAG53658.1; -.			
DR	HSSP; P30041; IPRX.			

DR	InterPro:	IPR000866;	AhpC-TSA.
DR	Pfam:	PF00578;	AhpC-TSA; 1.
SQ	SEQUENCE	199 AA;	22165 MW; BP9926D9F45E01D9 CMC64;
	Query Match	50.1%;	Score 721.5; DB 6; Length 199;
	Best Local Similarity	69.8%;	Pred. No. 2.8e-61;
	Matches 134;	Conservative 23;	Mismatches 34; Indels 1; Gaps 1;
OY	AKISRPADVMEGTAVI-DGEFEKELTPTVRGKYLVFFFPFLDPFTVCPTETIAAFGRLEE	137	
Dd	6 AKIGRAAOFRTATAMPQGFRKDLSLADKGIVVEFFYPDLDFTFVCPTEIIAEFDRAEE	65	
OY	138 FRSINTEVVACSVDSQPTHAMINPRROGGICGPRIPLDSLTHOISKDVGVLEDSGH	197	
Dd	66 FKLLKCYIGASVDSHFCFLHMINPKNKGCGAGPNILISA PKRTIQNDYGVLKADGI	125	
OY	198 TLRGCLFIIDDKGLFOITLNDLPVGRSDETLRLVAQFYDYDKHGECVPACKPGESYTII	257	
Dd	126 SERGFIEIDDKGILFOITINDLPVGSRVDET LRLVAQFDTDKHGECVPACKPGSDPIIK	185	
OY	258 PDDPAKLKVFPDK 269		
Dd	186 PDVQSKSEIFSK 197		
	RESULT 11		
ID	093241 PRELIMITARY:	PRT;	199 AA.
DC	093241;		
DT	01-NOV-1998 (TREMBLrel_08_Created)		
DT	01-NOV-1998 (TREMBLrel_08_Last sequence update)		
DT	01-DEC-2001 (TREMBLrel_19,		Last annotation update)
DE	Natural killer cell enhancing factor (Natural killer enhancer		
NEKEf).			
CN	Cyprinus carpio (Common carp).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
CC	Cyprinidae; Cyprinus.		
OX	NCBI_Taxid=7962;		
RN	[1]		
RA	"SEQUENCE FROM N.A.		
RA	Shin D., Fujiki K., Nakao M., Yano T.;		
RT	"cDNA cloning of a carp homologue of a human natural killer cell		
RT	enhancing factor";		
RN	Submitted (Feb-1998) to the EMBL/GenBank/DDBJ databases.		
RE	[2]		
RR	SEQUENCE FROM N.A.		
RA	Shin D., Fujiki K., Nakao M., Yano T.;		
RT	"Organization of the NEKF gene and its expression in the common carp		
RT	(Cyprinus carpio)."		
RU	Submitted (Sep-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AB010959; BAA32086.1; -.		
DR	EMBL; AB048789; BAB39202.1; -.		
HSSP:	P30041; IPRX.		
DR	InterPro: IPRO00866; Ahpc-TSA.		
DR	Pfam: PF00578; Ahpc-TSA; 1.		
SO	SEQUENCE 199 AA; 22196 MW; 3AB248CEB89CADA CRC64;		
	Query Match	50.1%;	Score 721.5; DB 13; Length 199;
	Best Local Similarity	69.9%;	Pred. No. 2.8e-61;
	Matches 135;	Conservative 20;	Mismatches 37; Indels 1; Gaps 1;
OY	78 KAKISRPAWEGTAVI-DGEFKELLTDIRNKYLVFPPYLDPTFCPTETIAFGDRLE	136	
Dd	5 KAHIKPAPADETKAWPDGDGFKDLSLSEYKGKYYLFEPFLDFPVCTETIAFSDAVE	64	
OY	137 EFERSINTEVACSVDSQPTHAMINTPRRGGIGPRIPLSLSDLTHOISKDVGYLEDNSG	196	
Dd	65 EFRKINCIVCASVDSHCFLHAMINTPKKGGLGMNVPLVADSIRTSODPGLVKEDBG	124	
OY	HTURGLEIIDDGKGLFQTILLNDLPVGRSVDDELRLVAQFYDYTDKHGEVCPAGMKPGSETI	256	

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,



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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:15:02 ; Search time 11 seconds

(without alignments)  
1021.826 million cell updates/sec

Title: US-09-911-346-2  
Perfect score: 1441  
Sequence: 1 MEALPLLAATTDPGHRRL.....GSEFIIPDPAGKLYEDKLN 271

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	1	PDX4_HUMAN
2	1296	89.9	274	1	PDX4_BOVIN
3	1262.5	87.6	274	1	PDX4_MOUSE
4	749	52.0	199	1	PDX2_BOVIN
5	746	51.8	198	1	PDX2_HUMAN
6	744	51.6	198	1	PDX2_RAT
7	735.5	51.0	199	1	PDX1_HUMAN
8	732	50.8	198	1	PDX1_MOUSE
9	731.5	50.8	200	1	PDX1_MOUSE
10	730.5	50.7	199	1	PDX1_MOUSE
11	721.5	50.1	199	1	PDX1_MOUSE
12	703	48.8	256	1	PDX3_HUMAN
13	691	48.0	257	1	PDX3_BOVIN
14	689	47.8	257	1	PDX3_MOUSE
15	667	46.3	199	1	PDX2_BRUMA
16	660	45.8	200	1	PDX1_MOUSE
17	639.5	44.4	226	1	PDX1_MOUSE
18	631.5	43.8	199	1	PDX1_MOUSE
19	592.5	41.1	210	1	PDX1_MOUSE
20	589	40.9	210	1	PDX1_MOUSE
21	588.5	40.8	210	1	PDX1_MOUSE
22	584	40.5	195	1	PDX1_MOUSE
23	582.5	40.4	265	1	PDX1_MOUSE
24	571	39.6	266	1	PDX1_MOUSE
25	570.5	39.6	200	1	PDX1_MOUSE
26	567	39.3	195	1	PDX1_MOUSE
27	561	38.9	229	1	PDX1_MOUSE
28	556.5	38.6	229	1	PDX1_MOUSE
29	548	38.0	199	1	PDX1_MOUSE
30	489	33.9	127	1	PDX2_PIG
31	479.5	33.3	233	1	PDX2_PIG
32	477	33.1	178	1	PDX2_PIG
33	404	28.0	198	1	PDX2_PIG

## ALIGNMENTS

RESULT 1	ID	PD4_HUMAN	STANDARD:	PRT:	271 AA.
AC	Q13162	PD4_HUMAN	Q13162		
DT	15-JUL-1998		(Rel. 36, Created)		
DT	15-JUL-1998		(Rel. 36, Last sequence update)		
DT	15-JUN-2002		(Rel. 41, Last annotation update)		
DE	Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase A0372)				
DE	(Thioredoxin-dependent peroxidase A0372) (Antioxidant enzyme A0372) (AOE37-2).				
DE	PRDX4.				
GN	PRDX4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE:98049564; PubMed:9388242;				
RA	Jin D.-Y., Chae H.Z., Rhee S.G., Jeang K.-T.;				
RT	"Regulatory role for a novel human thioredoxin peroxidase in NF-kappa B activation."				
RT	J. Biol. Chem. 272:30952-30961(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE:Brain;				
RA	Strausberg R.;				
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	OVEROXIDATION OF CYS-124.				
RA	Rabilloud T.;				
RL	Unpublished observations (JUL-2002).				
CC	-I- FUNCTION: Probably involved in redox regulation of the cell.				
CC	modulates the activation of NF-kappa-B in the cytosol by a				
CC	regulation of I-kappa-B-alpha phosphorylation.				
CC	-I- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked.				
CC	upon oxidation (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-245-SH of the				
CC	other subunit to form an intermolecular disulfide with a				
CC	concomitant homodimer formation. The enzyme may be subsequently				
CC	regenerated by reduction of the disulfide by thioredoxin.				
CC	-I- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-				
CC	124 (to Cys-SO3H) upon oxidative stress.				
CC	-I- SIMILARITY: BELONGS TO THE AHP/C/TSR FAMILY.				
CC	-----				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: U25182; AAB95175.1; -				
DR	EMBL: BC003609; AAH03609.1; -				

DR EMBL: BC007107; AAH07107.1; -;  
 DR EMBL: BC016770; AAH16770.1; -;  
 DR HSSP: P30041; 1PRX.  
 DR Genew: HGNC:17169; PRDX4.  
 DR MIM: 606506; -;  
 DR InterPro: IPR000866; Ahpc-TSA.  
 DR Pfam: PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.  
 FT ACT SITE 20  
 FT DOMAIN 124 124 POLY-LEU.  
 FT DISULFID 124 245 REDOX-ACTIVE.  
 SQ SEQUENCE 271 AA: 30540 MW: 7556580049PC60F CRC64;

Query Match 100.0%; Score 1441; DB 1; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-126;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRRLRLPLPLFLPAGAVQGWETERTREBECHFYAGGQVY 60  
 DB 1 MEALPLAATTPDHGRRLRLPLPLFLPAGAVQGWETERTREBECHFYAGGQVY 60  
 QY 61 PGEASRVADSHLSLHLSKAKISKRPAPWEGTAVIDGFEKELTDYRGKYLVEFFYPLDF 120  
 DB 61 PGEASRVADSHLSLHLSKAKISKRPAPWEGTAVIDGFEKELTDYRGKYLVEFFYPLDF 120  
 QY 121 TFCVPTETIAFGDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRPLSDL 180  
 DB 121 TFCVPTETIAFGDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRPLSDL 180  
 QY 181 THQISKRYGYLEDSGHTLGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240  
 DB 181 THQISKRYGYLEDSGHTLGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240  
 QY 241 HGEVCPAGMKPGSETTIPDPAGKLYFDKLN 271  
 DB 241 HGEVCPAGMKPGSETTIPDPAGKLYFDKLN 271

## RESULT 2

PDX4\_BOVIN STANDARD; PRT; 274 AA.

AC 09BGIZ;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 GN Peroxiredoxin 4 (EC 1.11.1.1-) (Prx-IV).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Leyens G., Donnay I., Knoops B.;  
 RT "Cloning of 4 new bovine-peroxiredoxins, and screening of the complete  
 RT peroxiredoxin family in different bovine tissues.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Probably involved in redox regulation of the cell.  
 CC Regulates the activation of NF-kappa-B in the cytosol by a  
 CC modulation of I-kappa-B-alpha phosphorylation (By similarity).  
 CC -1- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,  
 CC upon oxidation (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-127  
 CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-248-SH of the  
 CC other subunit to form an intermolecular disulfide with a  
 CC concomitant homodimer formation. The enzyme may be subsequently  
 CC regenerated by reduction of the disulfide by thioredoxin (By  
 CC similarity).  
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
 CC 127 (to Cys-SO3H) upon oxidative stress (By similarity).  
 CC

CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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 CC -----

DR EMBL: AF305563; AAG53660.1; -;  
 DR HSSP: P30041; 1PRX.  
 DR InterPro: IPR000866; Ahpc-TSA.  
 DR Pfam: PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.  
 FT ACT SITE 127 127 REDOX-ACTIVE.  
 FT DISULFID 127 248 INTERCHAIN (PARTIAL) (BY SIMILARITY).  
 SQ SEQUENCE 274 AA: 30741 MW: AE14176CF1C70E37 CRC64;

Query Match 89.9%; Score 1296; DB 1; Length 274;  
 Best Local Similarity 92.1%; Pred. No. 1.3e-112;  
 Matches 246; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 5 PLAATTPDHGRRLRLPLPLFLPAGAVQGWETERTREBECHFYAGGQVYGEA 64  
 DB 8 PLPPTATLAPGRSRKLLPLPLFLRAEAVKGEAEERTREBECHFYAGGQVYGEV 67  
 QY 65 SRVSVADSHLSLHLSKAKISKRPAPWEGTAVIDGFEKELTDYRGKYLVEFFYPLDFEVC 124  
 DB 68 SRVSVADSHLSLHLSKAKISKRPAPWEGTAVIDGFEKELTDYRGKYLVEFFYPLDFEVC 127  
 QY 125 PTEIIAFGRDLFEERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRPLSDLTHQI 184  
 DB 128 PTEIIAFGRDLFEERSINTEVACSVDSQFTHLAMINTPRROGSLGGINPLADLNHQI 187  
 QY 185 SKDGYVLEDSGHTLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKGEV 244  
 DB 188 SKDGYVLEDSGHTLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKGEV 247  
 QY 245 CPAGMKPGSETTIPDPAGKLYFDKLN 271  
 DB 248 CPAGMKPGSETTIPDPAGKLYFDKLN 274

## RESULT 3

PDX4\_MOUSE STANDARD; PRT; 274 AA.

AC 008807;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peroxiredoxin 4 (EC 1.11.1.1-) (Prx-IV) (thioredoxin peroxidase A0372)  
 DE (thioredoxin-dependent peroxidase A0372) (Antioxidant enzyme  
 DE A0E372).  
 GN PRDX4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=21121079; Pubmed=11229364;  
 RA Wong C.M., Chun A.C., Kok K.H., Zhou Y., Fung P.C., Kung H.F.,  
 RA Jiang K.-T., Jin D.-Y.;  
 RT "Characterization of human and mouse peroxiredoxin IV: evidence for  
 RT inhibition by Prx-IV of epidermal growth factor- and p53-induced  
 RT reactive oxygen species.";  
 RL Antioxid. Redox. Signal. 2:507-518(2000).  
 CC -1- FUNCTION: Probably involved in redox regulation of the cell.  
 CC Regulates the activation of NF-kappa-B in the cytosol by a  
 CC modulation of I-kappa-B-alpha phosphorylation.  
 CC -1- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,  
 CC



RA Levens G., Donnay I., Knoops B.;  
RT "Cloning of a new bovine peroxiredoxin, and screening of the complete  
peroxiredoxin family in different bovine tissues.";  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
CC  
CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces  
CC peroxides with reducing equivalents provided through the  
CC thioredoxin system. It is not able to receive electrons from  
CC glutaredoxin. May play an important role in eliminating peroxides  
CC generated during metabolism. Might participate in the signaling  
CC cascades of growth factors and tumor necrosis factor- $\alpha$  by  
CC regulating the intracellular concentrations of H(2)O(2).  
CC  
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By  
CC similarity).  
CC  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC  
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized  
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other  
CC subunit to form an intermolecular disulfide with a concomitant  
CC homodimer formation. The enzyme may be subsequently regenerated by  
CC reduction of the disulfide by thioredoxin (By similarity).  
CC  
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
CC 52 (to Cys-SO3H) upon oxidative stress (By similarity).  
CC  
CC -1- SIMILARITY: BELONGS TO THE AHP/C/TSA FAMILY.  
CC  
CC -----  
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RC TISSUE-Liver:

OS Homo sapiens (Human) .

CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;  
OC Mammalia: Eutheria: Primates: Catarrhini: Homidae: Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94193012; PubMed=8144038;  
RA Lin Y.-S., Cha M.-K., Kim H.-K., Kim I.-H.;  
RT "The thiol-specific antioxidant protein from human brain: gene  
RT cloning and analysis of conserved cysteine regions.";  
RL Gene 140:279-284(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94299283; PubMed=8026862;  
RA Shau H., Butterfield L.H., Chiu R., Kim A.;  
RT "Cloning and sequence analysis of candidate human natural killer-  
RT enhancing factor genes.";  
RL Immunogenetics 40:129-134(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 35-198 FROM N.A.  
RL Oberbauer I.;  
RN Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 17-25; 140-150 AND 163-185.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
RT Vandekerckhove J.;  
RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
RT protein database of normal human epidermal keratinocytes.";  
RL Electrophoresis 13:960-969(1992).  
RN [6]  
RP SEQUENCE OF 17-26 AND 93-103.  
RC TISSUE=Erythrocyte;  
RX MEDLINE=94147970; PubMed=8313871;  
RA Golaz O., Hughes G.J., Fuitiger S., Paquet N., Balroch A.,  
RA Paquelli C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
RA Balant L., Hochstrasser D.F.;  
RT "Plasma and red blood cell protein maps: update 1993.";  
RL Electrophoresis 14:1223-1231(1993).  
RN [7]  
RP SEQUENCE OF 17-26; 111-135 AND 140-157.  
RC TISSUE=Colon carcinoma;  
RX MEDLINE=9295306; PubMed=9150948;  
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
RT "A two-dimensional gel database of human colon carcinoma proteins.";  
RL Electrophoresis 18:605-613(1997).  
RN [8]  
RP OVEROXIDATION OF CYS-51.  
RX PubMed=11904290.  
RA Rabilloud T., Heller M., Gasnier F., Luche S., Rey C., Aebersold R.,  
RA Benhammed M., Louisot P., Linnard J.;  
RT "Proteomic analysis of cellular response to oxidative stress.  
RT Evidence for in vivo overoxidation of peroxiredoxins at their active  
RT site.";  
RL J. Biol. Chem. 277:19396-19401(2002).  
RN [9]  
RP FUNCTION: Involved in redox regulation of the cell. Reduces  
CC peroxides with reducing equivalents provided through the  
CC thioredoxin system. It is not able to receive electrons from  
CC glutaredoxin. May play an important role in eliminating peroxides  
CC generated during metabolism. Might participate in the signaling  
CC cascades of growth factors and tumor necrosis factor-alpha by  
CC regulating the intracellular concentrations of H(2)O(2).  
CC FUNCTION: Enhances natural killer (NK) cells activity.  
CC SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by  
CC similarity).  
CC SUBCELLULAR LOCATION: Cytoplasmic.  
CC MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized

CC	to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other
CC	subunit to form an intermolecular disulfide with a concomitant
CC	homodimer formation. The enzyme may be subsequently regenerated by
CC	reduction of the disulfide by thioredoxin.
CC	-1 MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC	51 (to Cys-SO <sub>3</sub> H) upon oxidative stress.
CC	-1 SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; 222548; CAAB0269.1; -
DR	EMBL; L19185; AAA50465.1; -
DR	EMBL; BC000452; AAH00452.1; -
DR	EMBL; BC003022; AAH03022.1; -
DR	EMBL; X82321; CA57764.1; -
DR	HSSP; P30041; 1PRX.
DR	SWISS-2DPAGE; P32119; HUMAN.
DR	Aarhus/Ghent-2DPAGE; 6116; IEF.
DR	Genev; HGNC:9353; PRDX2.
DR	MIM; 600538; -
DR	InterPro; IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
KW	Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT	ACT SITE 51 51
FT	DISULFID 51 172
FT	CONFLICT 59 66
FT	CONFLICT 82 82
FT	CONFLICT 105 105
FT	CONFLICT 120 120
FT	CONFLICT 175 175
FT	CONFLICT 180 180
SO	SEQUENCE 198 AA; 21892 MW; 1AC761D908B32B46 CRC64;
Query Match	51.8%; Score 746; DB 1; Length 198;
Best Local Similarity	70.5%; Pred. No. 6.9e-62;
Matches 136; Conservative 26; Mismatches 31; Indels 0; Gaps 0;	
QY	79 AKISKAPDYWGTAVIDGEKELKIDYRGKYLVEFFYPDLDFTEVCPEITTAFGDRLEEF 138
Db	6 ARIQGPADDFATAVDDAFKEVKLSDYKGYVLFEPDLDFTEVCPEITTAFSNRADF 65
QY	139 RSINTEVAVGCVDSQFTLAINTPRQCGGLPIRIPLSLDTLQISDVCVYLEDQSH 198
Db	66 KRLGGEVAVGVSQFTLAINTPRKGGLGPIPLIADVTRLSQVGLKTDGSA 125
QY	199 LRGLEIIDKSLIQLITLNDLPVGSVDETRLVQAQFYTRKHGEGCPAGKPGSETIIP 258
Db	126 YRGLEIIDGKGVLRQITVNDLPVGSVDALRLVQAQFYTDHGHVCAQKPGSDTIKP 185
QY	259 DPAGKLYFKDLN 271
Db	186 NVDSKEYFSKHN 198
RESULT 6	
PDX2_RAT	STANDARD; PRT; 198 AA.
AC	P35704;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Peroxioredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin-
DE	dependent peroxidase reductase 1) (Thiol-specific antioxidant protein)
DE	(TSA).
GN	PRDX2 OR TDPX1.
GN	Rattus norvegicus (Rat).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratus.  
 ON NCB1\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=9431629; PubMed=8041738;  
 RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;  
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian  
 brain: alkyl hydroperoxide reductase and thiol-specific antioxidant  
 define a large family of antioxidant enzymes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).  
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces  
 peroxides with reducing equivalents provided through the  
 thioredoxin system. It is not able to receive electrons from  
 glutaredoxin. May play an important role in eliminating peroxides  
 generated during metabolism. Might participate in the signaling  
 cascades of growth factors and tumor necrosis factor-alpha by  
 regulating the intracellular concentrations of H(2)O(2).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By  
 similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized  
 to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other  
 subunit to form an intermolecular disulfide with a concomitant  
 homodimer formation. The enzyme may be subsequently regenerated by  
 reduction of the disulfide by thioredoxin (By similarity).  
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
 51 (to Cys-SO3H) upon oxidative stress (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U06099; AAA19959.1; -;  
 DR HSPSP; P30041; 1PRX.  
 DR InterPro: IPR000866; AHPc-TSA.  
 DR Pfam: PF00578; AHPc-TSA; 1.  
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.  
 FT ACT\_SITE 51 51 REDOX-ACTIVE (BY SIMILARITY).  
 FT DISULFID 51 172 INTERCHAIN (PARTIAL) (BY SIMILARITY).  
 FT SEQUENCE 198 AA; 21784 MW; FC6ADB9B0E9C447B CRC64;  
 SQ  
 Query Match 51.6%; Score 744; DB 1; Length 198;  
 Best Local Similarity 71.0%; Pred. No. 1,1e-61;  
 Matches 137; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

DR 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-  
 DE dependent peroxide reductase 2) (Proliferation-associated protein PAG)  
 DE (Natural killer cell enhancing factor A) (NKEF-A).  
 GN PDX1 OR TDPX2 OR PAGB OR PAGC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCB1\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9326652; PubMed=8496166;  
 RA Prospero M.T., Terbus D., Karczinski I., Goubin G.;  
 RT "A human cDNA corresponding to a gene overexpressed during cell  
 RT proliferation encodes a product sharing homology with amoebic and  
 RT bacterial proteins.";  
 RL J. Biol. Chem. 268:11050-11056(1993).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 RX MEDLINE=94299283; PubMed=8026862;  
 RA Shau H., Butterfield L.H., Chiu R., Kim A.;  
 RT "Cloning and sequence analysis of candidate human natural killer-  
 RT enhancing factor genes.";  
 RL Immunogenetics 40:129-134(1994).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 RC TISSUE=Urinary bladder;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RP [4]  
 RP OVEROXIDATION OF CYS-52.  
 RA Rabilloud T.;  
 RL Unpublished observations (JUL-2002).  
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces  
 peroxides with reducing equivalents provided through the  
 thioredoxin system but not from glutaredoxin. May play an  
 important role in eliminating peroxides generated during  
 metabolism. Might participate in the signaling cascades of growth  
 factors and tumor necrosis factor-alpha by regulating the  
 intracellular concentrations of H(2)O(2).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By  
 similarity). May form heterodimers with AOR2.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- INDUCTION: Constitutively expressed in most human cells; is  
 induced to higher levels upon serum stimulation in untransformed  
 and transformed cells.  
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized  
 to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other  
 subunit to form an intermolecular disulfide with a concomitant  
 homodimer formation. The enzyme may be subsequently regenerated by  
 reduction of the disulfide by thioredoxin.  
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
 52 (to Cys-SO3H) upon oxidative stress.  
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.  
 CC -1- DATABASE: NAME=Atlas Genet. Cyto genet. Onco. Haematol.;  
 WWW="http://www.inbioogen.fr/services/chromancer/genes/PAGID266.html".  
 CC -----  
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 CC -----  
 DR EMBL: X67951; CAA48137.1; -;  
 DR EMBL: L19184; AAA50464.1; -;  
 DR EMBL: BC007063; AAH07063.1; -;  
 DR EMBL: BC021683; AAH21683.1; -;  
 DR PIR: S32099; S32099.  
 DR PIR: A46711; A46711.  
 DR HSPSP; P30041; 1PRX.



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CC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
CN NCB1_TaxID=8330;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Tabata T., Kamio K., Tajima T., Kaneda T., Suzuki A.;
RT "Pdg gene-like protein (ABP-25) of Cynops embryo: regional
RL distribution and gene expression during early embryogenesis.";
RL Roux's Arch. Dev. Biol. 204:400-405(1995).
CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
CC THROUGH THE THIOREDUXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
CC CONCENTRATIONS OF H(2)O(2) (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: THE CYS-52-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2). AND THE OXIDIZED CYS-52 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-173-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
CC REDUCED BY THIOREDUXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHP/C-TSA FAMILY.
CC -----
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CC -----
DR EMBL: D37808; BAA07054.1; -.
DR HSSP: P30041; IPRX.
DR InterPro: IPR000866; AHP-C-TSA.
DR Pfam: PF00578; AHP-C-TSA; 1.
KW Antioxidant.
FT ACT_SITE 52 52 BY SIMILARITY.
FT ACT_SITE 173 173 BY SIMILARITY.
SQ SEQUENCE 200 AA; 22339 MW; 55A2B0801D633990 CRC64;

Query Match 50.8%; Score 731.5; DB 1; Length 200;
Best Local Similarity 71.5%; Pred. No. 1.5e-60;
Matches 138; Conservative 22; Mismatches 32; Indels 1; Gaps 1;

QY 78 KAKISPAPEWEGTAVI-DGEFKELKLTDRGKYLVEFFYPDLDTFTVCPTETIAFGDRLE 136
DB 5 KAOIGKPAPEFOAKAVMGEGFEKIKLADYRGKYVFFFPYPLDFTVCPTETIARSDRAE 64
QY 137 EFRSINTEVAVCSVDSOFTHLAMINTPRROGGLGPIRIPPLSDLRHQISKDYGVLDESG 196
DB 65 EFRKNCGLIASVDSHCHLAWMTISRKEGLSMKIPLVADTRRTISODYGLAKEDEG 124
QY 197 HLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGMKSGSETI 256
DB 125 ISFRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGMKSGSETI 184
QY 257 IPPDAGKLKLYFDK 269
DB 185 KPDISKSKKEYFSK 197

RESULT 10
PDX1_RAT
ID PDX1_RAT STANDARD; PRT; 199 AA.
AC Q63716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-
dependent peroxidase reductase 2) (Heme-binding 23 kDa protein) (HBP23).

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GN PROX1 OR TDPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CN NCB1_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96027454; PubMed=7577926;
RA Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L.,
RA Nagae Y., Muller-Eberhard U.;
RT "Purification, characterization, and cloning of a heme-binding
RL protein (23 kDa) in rat liver cytosol.";
RL Biochemistry 34:13398-13406(1995).
CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity). May form heterodimers with AOP2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 52 (to Cys-SO3H) upon oxidative stress (By similarity).
CC -1- SIMILARITY: BELONGS TO THE AHP/C-TSA FAMILY.
CC -----
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CC -----
DR EMBL: D30035; BAA06275.1; -.
DR HSSP: P30041; IPRX.
DR InterPro: IPR000866; AHP-C-TSA.
DR Pfam: PF00578; AHP-C-TSA; 1.
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT ACT_SITE 52 52 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 52 173 INTERCHAIN (PARTIAL) (BY SIMILARITY).
SQ SEQUENCE 199 AA; 22109 MW; BDF2D4AB8A776DA CRC64;

Query Match 50.7%; Score 730.5; DB 1; Length 199;
Best Local Similarity 70.3%; Pred. No. 1.9e-60;
Matches 135; Conservative 24; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISPAPEWEGTAVI-DGEFKELKLTDRGKYLVEFFYPDLDTFTVCPTETIAFGDRLE 137
DB 6 AKIGHPASFKATAMVPGQGFQDLSYKGYVFFFPYPLDFTVCPTETIARSDRAE 65
QY 138 FRSINTEVAVCSVDSOFTHLAMINTPRROGGLGPIRIPPLSDLRHQISKDYGVLDESGH 197
DB 66 FRKNCQVIGASVDSHCHLAWMTISRKEGGLGPIRIPPLSDLRHQISKDYGVLDESGH 125
QY 198 HLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGMKSGSETI 257
DB 126 SFRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGMKSGSETI 185
QY 258 IPPDAGKLKLYFDK 269
DB 186 PDVNSKKEYFSK 197

RESULT 11
PDX1_MOUSE

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ID PDX1\_MOUSE STANDARD: PRT: 199 AA.  
 AC P35700.  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3)  
 DE (Macrophage 23 kDa stress protein).  
 GN PDX1 OR TDPX2 OR MSP23 OR PDXA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC MGI:TaxID=10090.  
 RX TISSUE=Peritoneal macrophage;  
 RX MEDLINE=93366771; PubMed=8360158;  
 RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K., Sugita Y., Bannai S.;  
 RT "Cloning and characterization of a 23-kDa stress-induced mouse peritoneal macrophage protein.";  
 RL J. Biol. Chem. 268:18633-18636(1993).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Osteoblast;  
 RX MEDLINE=94375405; PubMed=8089076;  
 RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann E.;  
 RT "Cloning and characterization of OSF-3, a new member of the MERS family, expressed in mouse osteoblastic cells.";  
 RL J. Biochem. 115:641-643(1994).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Liver;  
 RA Hino K., Sato H., Bannai S.;  
 RT "Characterization of mouse type I peroxiredoxin gene and pseudogenes.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system but not from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity). May form heterodimers with AOP2.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES; HIGH CONCENTRATION IN LIVER.  
 CC -1- INDUCTION: BY OXIDATIVE AND SULFHYDRYL-REACTIVE AGENTS.  
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).  
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52 (to Cys-SO3H) upon oxidative stress (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D16142; BAA03713.1; -  
 DR EMBL: D21252; BAA04796.1; -  
 DR EMBL: AB023564; BAA86992.1; -  
 DR EMBL: AB023560; BAA86992.1; JOINED.  
 DR EMBL: AB023561; BAA86992.1; JOINED.  
 DR EMBL: AB023562; BAA86992.1; JOINED.

DR EMBL: AB023563; BAA86992.1; JOINED.  
 DR PIR: A48513; A48513.  
 DR PIR: JC2259; JC2259.  
 DR HSSP: P30041; 1PRX.  
 DR SWISS-2DPAGE: P35700; MOUSE.  
 DR MGI:99523; PDX1.  
 DR InterPro: IPR000866; AHPc-TSA.  
 DR Pfam: PF00578; AHPc-TSA; 1.  
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.  
 FT ACT\_SITE 52  
 FT DISULFID 52 173  
 FT SEQUENCE 199 AA; 22176 MW; BEF5C993A86124D1 CRC64;  
 SO  
 Query Match 50.1%; Score 721.5; DB 1; Length 199;  
 Best Local Similarity 68.8%; Pred. No. 1.3e-59;  
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;  
 QY 79 AKISKPAPYMEGTAI-DGEKELKLDYRGKYLVEFFYPPLDFTFVCPTEIIAFGRLEE 137  
 DB 6 AKIGPAPNFKATVMPDQGFKDLSLEYKGYVFFFPPLDFTFVCPTEIIAFSDRADE 65  
 QY 138 FRSINTEVYACSVDSQFHLAMINPRROGGLGPIRPLSDLTHQSKDGVYLEDSGH 197  
 DB 66 FKLLNCOVIGASVDSHFECHLAWINTPKRGGLGPMNIPILSDPKRTTAQDGVLEKADEGI 125  
 QY 198 TLRGFIIDDKGILRLITLNDLPYGRSVDETLRLVQAFQYDKAGENCAPAGMKPGSETII 257  
 DB 126 SFRGFIIDDKGILRLITLNDLPYGRSVDETLRLVQAFQYDKAGENCAPAGMKPGSDIIR 185  
 QY 258 PDPAKGLKYEFDK 269  
 DB 186 PDVNSKSEYFSK 197  
 RESULT 12  
 ID PDX3\_HUMAN STANDARD: PRT: 256 AA.  
 AC P30048; P35690; Q13776; Q96HK4;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein homolog) (HBC189) (PRX III).  
 GN PRDX3 OR AOP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NC MGI:TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95251598; PubMed=7733872;  
 RA Tsuji K., Copeland N.G., Jenkins N.A., Obinata M.;  
 RT "Mammalian antioxidant protein complements alkyldihydroperoxide reductase (ahpc) mutation in Escherichia coli.";  
 RL Biochem. J. 307:377-381(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin, Testis, Urinary bladder, and Uterus;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 148-240 FROM N.A.  
 RX MEDLINE=94108427; PubMed=7506601;  
 RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;  
 RT "A molecular inventory of human pancreatic islets: sequence analysis of 1000 cDNA clones.";  
 RL Hum. Mol. Genet. 2:1793-1798(1993).  
 RN [4]  
 RP SEQUENCE OF 63-72.  
 RC TISSUE=Liver;  
 RX MEDLINE=93162045; PubMed=1286669;

RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.:  
RT "Human liver protein map: a reference database established by  
RT microsequencing and gel comparison."  
RL Electrophoresis 13:992-1001(1992).  
RN [5]  
RP OXIDATION OF CYS-108.  
RA Rabilloud T.:  
CC Unpublished observations (JUL-2002).  
CC -1- FUNCTION: Involved in redox regulation of the cell. Protects  
CC radical-sensitive enzymes from oxidative damage by a radical-  
CC generating system.  
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-108  
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-229-SH of the  
CC other subunit to form an intermolecular disulfide with a  
CC concomitant homodimer formation. The enzyme may be subsequently  
CC regenerated by reduction of the disulfide by thioredoxin.  
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
CC 108 (to Cys-SO<sub>3</sub>H) upon oxidative stress.  
CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.  
CC -----  
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CC -----  
DR EMBL: DA9396; BAA08389.1; -;  
DR EMBL: BC002685; AAH02685.1; -;  
DR EMBL: BC008038; AAH08038.1; -;  
DR EMBL: BC008435; AAH08435.1; -;  
DR EMBL: BC021691; AAH21691.1; -;  
DR EMBL: BC022373; AAH22373.1; -;  
DR EMBL: T10952; -; NOT\_ANNOTATED\_CDS.  
DR SWISS-2DPAGE: P30048; HUMAN.  
DR SlenA-2DPAGE: P30048; -;  
DR Genew: HGNC:9354; PRDX3.  
DR MIM: 604769; -;  
DR InterPro: IPR000866; AhpC-TSA.  
DR Pfam: PF00578; AhpC-TSA; 1.  
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;  
KW Mitochondrion; Transit peptide.  
FT TRANSIT 1 62 MITOCHONDRION.  
FT CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.  
FT ACT\_SITE 108 108 REDOX-ACTIVE.  
FT DISULFID 108 229 INTERCHAIN (PARTIAL) (BY SIMILARITY).  
FT CONFLICT 31 31 R -> W (IN REF. 2; AAH08435).  
SQ SEQUENCE 256 AA; 27692 MW; 8BBE7F5E5BEE9BE CRC64;  
Query Match 48.8%; Score 703; DB 1; Length 256;  
Best Local Similarity 66.5%; Pred. No. 9.1e-58;  
Matches 12; Conservative 26; Mismatches 36; Indels 0; Gaps 0;

DB 245 AASKEFGKVN 255  
RESULT 13  
PDX3\_BOVIN STANDARD; PRT; 257 AA.  
AC P35705;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC  
DE 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22  
DE protein).  
GN PRDX3 OR AOP1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_Taxid=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Adrenal medulla;  
RX MEDLINE=97069947; PubMed=8912927;  
RA Hiroi T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.;  
RT "The cDNA sequence encoding bovine SP-22, a new defence system  
RT against reactive oxygen species in mitochondria."  
RL DNA Seq. 6:239-242(1996).  
RN [2]  
RP SEQUENCE OF 2-257 FROM N.A.  
RC TISSUE=Adrenal medulla;  
RX MEDLINE=94375407; PubMed=8089078;  
RA Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.;  
RT "Purification and characterization of a substrate protein for  
RT mitochondrial ATP-dependent protease in bovine adrenal cortex."  
RL J. Biochem. 115:648-654(1994).  
CC -1- FUNCTION: Involved in redox regulation of the cell. Protects  
CC radical-sensitive enzymes from oxidative damage by a radical-  
CC generating system.  
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-109  
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the  
CC other subunit to form an intermolecular disulfide with a  
CC concomitant homodimer formation. The enzyme may be subsequently  
CC regenerated by reduction of the disulfide by thioredoxin (by  
CC similarity).  
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-  
CC 109 (to Cys-SO<sub>3</sub>H) upon oxidative stress (by similarity).  
CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: D82025; BAA1511.1; -;  
DR HSP: P30041; IPRX.  
DR InterPro: IPR000866; AhpC-TSA.  
DR Pfam: PF00578; AhpC-TSA; 1.  
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;  
KW Mitochondrion; Transit peptide.  
FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).  
FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.  
FT ACT\_SITE 109 109 REDOX-ACTIVE (BY SIMILARITY).  
FT DISULFID 109 230 INTERCHAIN (PARTIAL) (BY SIMILARITY).  
SQ SEQUENCE 257 AA; 28195 MW; F2E89E2F12A42D CRC64;  
Query Match 48.0%; Score 691; DB 1; Length 257;  
Best Local Similarity 65.4%; Pred. No. 1.2e-56;



Matches 125; Conservative 28; Mismatches 38; Indels 0; Gaps 0;

QY 81 ISKPAPYMEBTAVIDGFEKELKTDYRGKYLVEFFYPLDFTVCPEITIAFGRLFEFRS 140  
 Db 66 VTQHAHYEFGTAVVNGEFEKELSLDDEKFKYLVLFYPLDFTVCPEITIAFGSKAEFND 125  
 QY 141 INTEVAVACVDSQFTHLAMIINTPRROGCGPIRIPILSLDTHQISKDGVYLEDGHTLR 200  
 Db 126 VNCVAVAVSDSHFSLHAMIINTPRKNNGGLGHMIALSLDKOISRDCVGLLEPGCLALR 185  
 QY 201 GLEIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGVCPCAGKPGSEITIPDP 260  
 Db 186 GLEIIDPNCVIVKHLVNDLPVGRSVDETLRLVKAFQVETHEGVCPCANWTPESPITIKRSP 245  
 QY 261 AGKLYEPKLN 271  
 Db 246 TASREYFEKVN 256

## RESULT 14

PDX3\_MOUSE STANDARD; PRT; 257 AA.

AC P20108;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Thiorodoxin-dependent peroxidase, mitochondrial precursor (EC 1.11.1.-) (Peroxidoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein) (PRX III).  
 DE PDX3 OR AOP1 OR MERS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBL\_TaxID=10090;  
 RN [1]  
 RP MEDLINE=90060782; Pubmed=2583515;  
 RX Yamamoto T., Matsui Y., Natori S., Obinata M.;  
 RA "Cloning of a housekeeping-type gene (MERS) preferentially expressed in murine erythroleukemia cells.";  
 RL Gene 80:337-343(1989).  
 CC -1- FUNCTION: Involved in redox regulation of the cell. Protects radical-sensitive enzymes from oxidative damage by a radical-generating system.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
 CC -1- TISSUE SPECIFICITY: Housekeeping-type gene preferentially expressed in murine erythroleukemia (MEL) cells.  
 CC -1- INDUCTION: Expression is increased after induction of MEL cells to differentiation by DMSO.  
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-109 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thiorodoxin (By similarity).  
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-109 (to Cys-SO<sub>3</sub>H) upon oxidative stress (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE AHP/C/TSFA FAMILY.  
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 CC EMBL: M28723; AAA39524.1; -  
 CC PIR: J00064; J00064.  
 CC MGD: MGI:88034; Prdx3.  
 CC InterPro: IPR000866; AhpC-TSA.

DR Pfam: PF00578; Ahpc-TSA: 1.  
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;  
 KM Mitochondrion; Transil peptide.  
 FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).  
 FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.  
 FT ACT\_SITE 109 109 REDOX-ACTIVE (BY SIMILARITY).  
 FT DISULFID 109 230 INTERCHAIN (PARTIAL) (BY SIMILARITY).  
 SQ SEQUENCE 257 AA; 28127 MW; 65513F2C5F1D56C0 CRC64;

Query Match 47.8%; Score 689; DB 1; Length 257;  
 Best Local Similarity 64.4%; Pred. No. 1.8e-56;

Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAPYMEBTAVIDGFEKELKTDYRGKYLVEFFYPLDFTVCPEITIAFGRLFEFRS 140  
 Db 66 VTQHAHYEFGTAVVNGEFEKELSLDDEKFKYLVLFYPLDFTVCPEITIAFGSKAEFND 125  
 QY 141 INTEVAVACVDSQFTHLAMIINTPRROGCGPIRIPILSLDTHQISKDGVYLEDGHTLR 200  
 Db 126 VNCVAVAVSDSHFSLHAMIINTPRKNNGGLGHMIALSLDKOISRDCVGLLEPGCLALR 185  
 QY 201 GLEIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGVCPCAGKPGSEITIPDP 260  
 Db 186 GLEIIDPNCVIVKHLVNDLPVGRSVDETLRLVKAFQVETHEGVCPCANWTPESPITIKRSP 245  
 QY 261 AGKLYEPKLN 271  
 Db 246 TASREYFEKVN 256

## RESULT 15

TDX2\_BRUMA STANDARD; PRT; 199 AA.

AC Q17172;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Thiorodoxin peroxidase 2 (Thiorodoxin-dependent peroxidase reductase 2) (thiol-specific antioxidant protein 2).  
 DE T5A2.  
 OS Brugia malayi.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.  
 NC NCBL\_TaxID=6279;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ghosh I., Raghavan N., Blaxter M., Scott A.L.;  
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP REVISIONS TO 176-189.  
 RA Scott A.L., Ghosh I., Raghavan N., Blaxter M.;  
 RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR CONCENTRATIONS OF H(2)O(2) (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- PTM: THE CYS-53-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY H(2)O(2), AND THE OXIDIZED CYS-53 (PROBABLY CYS-SOH) RAPIDLY REACTS WITH CYS-174-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE AHP/C/TSFA FAMILY.  
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EMBL: U47100; AAB67873.1; -  
HSP; P30041; IPX.  
InterPro: IPR000866; Ahpc-TSA.  
Pfam: PF00578; Ahpc-TSA; 1.  
Antioxidant.  
ACT\_SITE 53 53 BY SIMILARITY.  
ACT\_SITE 174 174 BY SIMILARITY.  
SEQUENCE 199 AA; 22042 MW; 8932BD8898B271B CRC64;

Query Match 46.3%; Score 667; DB 1; Length 199;  
Best Local Similarity 63.7%; Pred. No. 1.4e-54;

Matches 123; Conservative 26; Mismatches 44; Indels 0; Gaps 0;

QY 77 SKAKISKPAWEGTAVNIDGEEKELKLTIDYRGKYLVEFFYPPLDFTFVCPTEIIAFGDRLE 136  
DB 6 SKAFIQPAPNFKFTAVVNGDFKEISLGQFKGYVLLFYPPLDFTFVCPTEIIAFSDRIA 65  
QY 137 EFRSINTEVYACVSQFTFLAMINTPRQGGIGPIRIPPLSDLNQISKDYGVLLEDG 196  
DB 66 EFKOLDVAVMACSTDHFSHFLAMVNTDRKMGIGQMNPILAYTNHVISRAVGVLKEDG 125  
QY 197 HTLRGLFIIDDKGILBOITLNDLPVGRSVDETILVQAFQYTDKHGECVCPAGKPGSETI 256  
DB 126 IAYRGLEITDPKGIIGQITINDLPVGRSVDETILVQAFQYTDKHGECVCPAGKPGSETI 185  
QY 257 IPPPAGKLYFDK 269  
DB 186 KPGVKESKAYFEK 198

Search completed: January 17, 2003, 19:17:39  
Job time : 17 secs

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